

## SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

### Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

### STAFF USE ONLY

Date completed: 3/24  
Searcher: Sch... 777-2536  
Terminal time: 7  
Elapsed time: 12  
CPU time: \_\_\_\_\_  
Total time: \_\_\_\_\_  
Number of Searches: \_\_\_\_\_  
Number of Databases: \_\_\_\_\_

Search Site  
\_\_\_\_ STIC  
\_\_\_\_ ~~CM-1~~ *Perman*  
\_\_\_\_ Pre-S  
Type of Search  
\_\_\_\_ 2 N.A. Sequence  
\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

Vendors  
\_\_\_\_ IG  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
\_\_\_\_ ✓ Other *Complan*

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

M nucleic - nucleic search, using sw model

un on: March 21, 2004, 21:05:39 ; Search time 237 Seconds  
(without alignments)  
12937.146 Million cell updates/sec

Title: US-09-515-806A-1  
Effect score: 5525  
Sequence: 1 tgcggccacgcgtccgacc.....aatgtttcatatccctgca 5525

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:  
1: /cgn2\_6/ptodata/2/ina/5A COMB.seq.\*  
2: /cgn2\_6/ptodata/2/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/2/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/2/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	244	4.4	244	US-09-016-434-785	Sequence 785, Appl
2	187.6	3.4	81001	US-09-520-580-1	Sequence 1, Appl
3	185.6	3.4	15297	US-09-617-180-3	Sequence 3, Appl
4	185.6	3.4	15297	US-09-617-180-3	Sequence 3, Appl
5	185.6	3.4	176373	US-10-003-295-3	Sequence 17, Appl
6	181.2	3.3	44848	US-09-428-155-17	Sequence 42, Appl
7	179	3.2	59065	US-09-435-739-42	Sequence 3, Appl
8	179	3.2	59065	US-09-813-817-3	Sequence 3, Appl
9	177.6	3.2	3166	US-09-978-197-3	Sequence 8, Appl
10	177.2	3.2	4079	US-09-341-587-8	Sequence 1449, Ap
11	176.8	3.2	81001	US-09-016-434-1449	Sequence 1, Appl
12	176.2	3.2	6769	US-09-750-580-1	Sequence 20, Appl
13	176.2	3.2	6769	US-09-480-784-20	Sequence 20, Appl
14	176.2	3.2	6769	US-08-483-553-20	Sequence 20, Appl
15	176.2	3.2	6769	US-08-487-002-20	Sequence 20, Appl
16	176.2	3.2	6769	US-08-483-554B-20	Sequence 20, Appl
17	176.2	3.2	6769	US-08-488-011B-20	Sequence 20, Appl
18	176.2	3.2	6769	US-08-850-727-20	Sequence 20, Appl
19	176.2	3.2	6769	PCT-US93-10203-20	Sequence 20, Appl
20	176.2	3.2	6769	PCT-US93-10203-20	Sequence 20, Appl
21	175.8	3.2	21784	US-09-820-002-3	Sequence 3, Appl
22	175.8	3.2	55298	US-09-491-356C-1	Sequence 1, Appl
23	175.4	3.2	9365	US-09-608-285A-8	Sequence 8, Appl
24	175.4	3.2	9365	US-09-350-836B-8	Sequence 8, Appl
25	175.4	3.2	9365	US-09-370-265-8	Sequence 8, Appl
26	175.4	3.2	9365	US-09-557-800C-8	Sequence 8, Appl
27	175.4	3.2	9365	US-09-370-625A-8	Sequence 8, Appl

Query Match 4.4%; Score 244; DB 4; Length 244;  
Best Local Similarity 100.0%; Pred. No. 5.7e-52;

ALIGNMENTS

RESULT 1

US-09-016-434-785  
; Sequence 785, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREMITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0002 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 785:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 244 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: HNT2AGT01  
; CLONE: 48B190  
; US-09-016-434-785

Sequence 42, Appl  
Sequence 42, Appl  
Sequence 59, Appl  
Sequence 3, Appl  
Sequence 1, Appl  
Sequence 7, Appl  
Sequence 4, Appl  
Sequence 43, Appl  
Sequence 43, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 1, Appl  
Sequence 6, Appl  
Sequence 10, Appl  
Sequence 1801, Ap  
Sequence 1801, Ap

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Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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2b 1 CAGAAATCAGATGAAGATTCATGAAAGAAATGCGTCCATGAAAGTGAGCCATCAGTG 60
2Y 2433 ACAGCTCAGGCTGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAGGACACTTTA 2492
2b 61 ACAGCTCAGGCTGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAGGACACTTTA 120
2Y 2493 CGAGACACCAATGACAGGAGCTGTATCGAGAGACCGTCAGACTCTGGAGGCTTTTGA 2552
2b 121 CGAGACACCAATGACAGGAGCTGTATCGAGAGACCGTCAGACTCTGGAGGCTTTTGA 180
2Y 2553 GAGATTCGATGATGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGATTTGAAG 2612
2b 181 GAGATTCGATGATGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGATTTGAAG 240
2Y 2613 CCTG 2616
2b 241 CCTG 244

RESULT 2
US-09-750-580-1/c
; Sequence 1, Application US/09750580
; Patent No. 6455280
; GENERAL INFORMATION:
; APPLICANT: Yen, Frances
; APPLICANT: Denison, Blake
; APPLICANT: Bour, Barbara
; APPLICANT: Bihain, Bernard
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Ebbets-Reed, Dana
; APPLICANT: Salter-Cid, Luisa
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
; FILE REFERENCE: 89 US2 CIP
; CURRENT APPLICATION NUMBER: US/09/750,580
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/599,362
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB00/0101
; PRIOR FILING DATE: 2000-06-21
; PRIOR APPLICATION NUMBER: PCT/IB99/02058
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: US 49/459/099
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: US 60/113,686
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: US 60/141,032
; PRIOR FILING DATE: 1999-06-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent.Pm
; SEQ ID NO 1
; LENGTH: 81001
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10946..12946
; OTHER INFORMATION: 5'regulatory region
; NAME/KEY: exon
; LOCATION: 12947..12958
; OTHER INFORMATION: exon 1
; NAME/KEY: exon
; LOCATION: 13470..13526
; OTHER INFORMATION: exon 2
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; LOCATION: 13641..13752
; OTHER INFORMATION: exon 3
; NAME/KEY: exon
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; NAME/KEY: allele
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; NAME/KEY: allele
; LOCATION: 12347
; OTHER INFORMATION: 17-42-319 : polymorphic base C or T
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; OTHER INFORMATION: 17-41-250 : polymorphic base C or T
; NAME/KEY: allele
; LOCATION: 42218
; OTHER INFORMATION: 20-841-149 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 45442
; OTHER INFORMATION: 20-842-115 : polymorphic base A or G
; NAME/KEY: allele
; LOCATION: 77058
; OTHER INFORMATION: 20-853-415 : polymorphic base C or T
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; LOCATION: 929..949
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; NAME/KEY: primer_bind
; LOCATION: 1357..1377
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; LOCATION: 12029..12050
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; OTHER INFORMATION: 17-42.rp complement
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; NAME/KEY: primer_bind
; LOCATION: 77166..77185
; OTHER INFORMATION: 20-853.rp complement
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; OTHER INFORMATION: 17-42-319.mis
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; LOCATION: 12348..12366
; OTHER INFORMATION: 17-42-319.mis complement
; NAME/KEY: primer_bind
; LOCATION: 15222..15240
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NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
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NAME/KEY: misc binding
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LOCATION: 12335..12359
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NAME/KEY: misc binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42205..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77045..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
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3.4%; Score 187.6; DB 4; Length 81001;
Best Local Similarity
71.1%; Pred. No. 3.2e-36;
Matches 263; Conservative 0; Mismatches 104; Indels 3; Gaps 1;
Qy 5084 TCATCATATTTTAAATTAATTTCTAAGAAGAGGCTGGGTGAGTGGCTCACACCTTTAA 5143
Db 65068 TTACCTGATTTTACAAATAAGAAATGTTGTGGCCAGTGCAGTGGCTCACGCTGTAA 65009
Qy 5144 TCCAGACATTTGGGAAGCAAGGAGGAGTCTGTTGAACCAAGGAGTTGAGACCAG 5203
Db 65008 TCCAGACATTTGGGAGGCAAGGTTGGTGGATCATCCTGAGTCCAGGAGTTGAGACCAG 64949
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Db 64948 CTTGGCCACATGTTGAACCCCGTCTCTATTAAAAATACAAAAATTAAGCCGGCATGGT 64889
Qy 5264 GGCACATGCTGTAGTCCAGCTACTCCAGGCTGAG---ATGATCATCTGAGCTCA 5320
Db 64888 GGCAGGAGGCTGTAAATCCAGCTACTCAGGAGGCTGAGGCGAGGAGATCATCTTGAACCG 64829
Qy 5321 GGAGGTTGAGCTGGCAGTGCAGTGTGACTCGCCCACTCACTCCAGTCTGGGACACAGA 5380
Db 64828 GGAGGCGGAGTTGCACTGAGCTGAGATTGCCACTCACTCCAGCTGAGGAGCAAGA 64769
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Db 64768 GCGAGACTCTGTATCAAAAAAATAAATAAATAAGGAAATCTGTGGCTCAG 64709
Qy 5441 CAAAGTTGAG 5450
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NAME/KEY: primer_bind
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NAME/KEY: primer_bind
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NAME/KEY: primer_bind
LOCATION: 77059..77077
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NAME/KEY: misc binding
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LOCATION: 12335..12359
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NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77045..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
Query Match
3.4%; Score 187.6; DB 4; Length 81001;
Best Local Similarity
71.1%; Pred. No. 3.2e-36;
Matches 263; Conservative 0; Mismatches 104; Indels 3; Gaps 1;
Qy 5084 TCATCATATTTTAAATTAATTTCTAAGAAGAGGCTGGGTGAGTGGCTCACACCTTTAA 5143
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Db 65008 TCCAGACATTTGGGAGGCAAGGTTGGTGGATCATCCTGAGTCCAGGAGTTGAGACCAG 64949
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Db 64948 CTTGGCCACATGTTGAACCCCGTCTCTATTAAAAATACAAAAATTAAGCCGGCATGGT 64889
Qy 5264 GGCACATGCTGTAGTCCAGCTACTCCAGGCTGAG---ATGATCATCTGAGCTCA 5320
Db 64888 GGCAGGAGGCTGTAAATCCAGCTACTCAGGAGGCTGAGGCGAGGAGATCATCTTGAACCG 64829
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NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
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LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77045..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
Query Match
3.4%; Score 187.6; DB 4; Length 81001;
Best Local Similarity
71.1%; Pred. No. 3.2e-36;
Matches 263; Conservative 0; Mismatches 104; Indels 3; Gaps 1;
Qy 5084 TCATCATATTTTAAATTAATTTCTAAGAAGAGGCTGGGTGAGTGGCTCACACCTTTAA 5143
Db 65068 TTACCTGATTTTACAAATAAGAAATGTTGTGGCCAGTGCAGTGGCTCACGCTGTAA 65009
Qy 5144 TCCAGACATTTGGGAAGCAAGGAGGAGTCTGTTGAACCAAGGAGTTGAGACCAG 5203
Db 65008 TCCAGACATTTGGGAGGCAAGGTTGGTGGATCATCCTGAGTCCAGGAGTTGAGACCAG 64949
Qy 5204 CTTGAGCAACAAAGCAAGACCCCTCTCTATAAAAACTAAAAAATTAAGTTGGGCATGGT 5263
Db 64948 CTTGGCCACATGTTGAACCCCGTCTCTATTAAAAATACAAAAATTAAGCCGGCATGGT 64889
Qy 5264 GGCACATGCTGTAGTCCAGCTACTCCAGGCTGAG---ATGATCATCTGAGCTCA 5320
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64708 ACGATTTAAG 64699
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
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OTHER INFORMATION: 20-842-115.mis
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OTHER INFORMATION: 20-842-115.mis complement
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OTHER INFORMATION: 20-853-415.mis
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OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc binding
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NAME/KEY: misc binding
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc binding
LOCATION: 42205..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc binding
LOCATION: 77045..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1
Query Match
3.4%; Score 187.6; DB 4; Length 81001;
Best Local Similarity
71.1%; Pred. No. 3.2
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Qy 5441 CAAAGTTGAG 5450  
D<sub>b</sub> 64708 AGAAGTTAAG 6469



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RESULT 6
US 09-435-739-42/c
; Sequence 42, Application US/09435739
; Patent No. 6654105
;
; GENERAL INFORMATION:
; APPLICANT: Packer, Iris
; APPLICANT: Puckavsky, Israel
; APPLICANT: Puckavsky, Elena
; APPLICANT: Puckavsky, Elena
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY
; TITLE OF INVENTION: EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

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[illegible]

RESULT 7  
US-09-813-817-3  
; Sequence 3, Application US/09813817  
; Patent No. 6340583  
; GENERAL INFORMATION:

APPLICANT: YAN, Chunhua et al.  
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
TITLE OF INVENTION: THEREOF  
FILE REFERENCE: CL001178  
CURRENT APPLICATION NUMBER: US/09/813,817  
CURRENT FILING DATE: 2001-03-22  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 59065  
TYPE: DNA  
ORGANISM: Human  
US-09-813-817-3

Query Match 3.2%; Score 179; DB 4; Length 59065;  
Best Local Similarity 74.3%; Pred. No. 3.9e-34;  
Matches 240; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

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b 32283 ACATTTAATCCTCACTCCAGGCCAGGCATAGTGGCTCAGCACTGTAAATCCAGCACTTCG 32342

Y 5157 GGAAGCCAAAGCAGCAAGACTGCTTGAACCCAGGAGTTTGAGACCACTTGAGCAACAAA 5216  
b 32343 GGAGCCAAAGCGCGGAGATCACTTGAGTGGAGTTTGAGACCACTTGAGCAACATG 32402

Y 5217 GCAAGACCCCTCTCTATAAACTAAATAATAGTTGGCATGTTGGCATGCTCTGT 5276  
b 32403 GGGAAACCCCTCTCTATAAACTAAATAATAGTTGGCATGTTGGCATGCTCTGT 32462

Y 5277 AGTCCAGCTACTCCAGAGCGTGGATGG---ATCATCTGAGCCTCAGGAGTTGAGCT 5333  
b 32463 AATCCAGCTACTCCAGAGCGTGGATGG---ATCATCTGAGCCTCAGGAGTTGAGCT 32522

Y 5334 GCAGTGAGCTGTGACTGCGCACTGCTGAGTGGCACTGCTGGCAACAGCAAGCCCTGTC 5393  
b 32523 GCAGTGAGCGGAGATTGTGCGCACTGCTGAGTGGCACTGCTGGCAACAGCAAGCCCTGTC 32582

Y 5394 TTAATAAAAGAAAAA 5416  
b 32583 TCAATAAAAGAAAAAAGAA 32605

RESULT 8  
US-09-978-197-3  
; Sequence 3, Application US/09978197  
; Patent No. 6403353  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001178  
; CURRENT APPLICATION NUMBER: US/09/978,197  
; CURRENT FILING DATE: 2001-10-17  
; PRIOR APPLICATION NUMBER: 09/813,817  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 59065  
; TYPE: DNA  
; ORGANISM: Human  
US-09-978-197-3

Query Match 3.2%; Score 179; DB 4; Length 59065;  
Best Local Similarity 74.3%; Pred. No. 3.9e-34;  
Matches 240; Conservative 0; Mismatches 80; Indels 3; Gaps 1;

Y 5097 AATTAAATCTTAAGAGAGCGTGGTGGAGTGGCTCAGCTTAAATCCAGCACTTTG 5156  
b 32283 ACATTTAATCCTCACTCCAGGCCAGGCATAGTGGCTCAGCACTGTAAATCCAGCACTTCG 32342

QY 5157 GGAAGCCAAAGCAGCAAGACTGCTTGAACCCAGGAGTTTGAGACCACTTGAGCAACAAA 5216  
Db 32343 GGAGCCAAAGCGCGGAGATCACTTGAGTGGAGTTTGAGACCACTTGAGCAACATG 32402

QY 5217 GCAAGACCCCTCTCTATAAACTAAATAATAGTTGGCATGTTGGCATGCTCTGT 5276  
Db 32403 GGGAAACCCCTCTCTATAAACTAAATAATAGTTGGCATGTTGGCATGCTCTGT 32462

QY 5277 AGTCCAGCTACTCCAGAGCGTGGATGG---ATCATCTGAGCCTCAGGAGTTGAGCT 5333  
Db 32463 AATCCAGCTACTCCAGAGCGTGGATGG---ATCATCTGAGCCTCAGGAGTTGAGCT 32522

QY 5334 GCAGTGAGCTGTGACTGCGCACTGCTGAGTGGCACTGCTGGCAACAGCAAGCCCTGTC 5393  
Db 32523 GCAGTGAGCGGAGATTGTGCGCACTGCTGAGTGGCACTGCTGGCAACAGCAAGCCCTGTC 32582

QY 5394 TTAATAAAAGAAAAA 5416  
Db 32583 TCAATAAAAGAAAAAAGAA 32605

RESULT 9  
US-09-341-587-8/c  
; Sequence 8, Application US/09341587  
; Patent No. 6345606  
; GENERAL INFORMATION:  
; APPLICANT: Mollenhauer, Jan  
; TITLE OF INVENTION: Protein Containing an SRCR Domain  
; FILE REFERENCE: 4121-108  
; CURRENT APPLICATION NUMBER: US/09/341,587  
; CURRENT FILING DATE: 1999-08-31  
; EARLIER APPLICATION NUMBER: PCT/DE98/00096  
; EARLIER FILING DATE: 1998-01-09  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 3166  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-341-587-8

Query Match 3.2%; Score 177.6; DB 4; Length 3166;  
Best Local Similarity 76.9%; Pred. No. 1.6e-34;  
Matches 243; Conservative 0; Mismatches 69; Indels 4; Gaps 2;

QY 5102 AATTTCTAAGAGAGCGTGGTGGAGTGGCTGCAGTGGCTCACACCTTTAATCCAGCACTTTGGGAAG 5161  
Db 888 AAGCTCAGAAAGAGCGCGGTGCAGTGGCTCACACCTGTAAATCCCGGCACCTTTGGGAGG 829

QY 5162 CCAAGGAGGAGAGCTGCTTGAACCCAGGAGTTTGAGACCACTTGAGCAAGCAACAAAGCAG 5221  
Db 828 CCTAGGAGGAGAGCTGCTTGAACCCAGGAGTTTGAGACCACTTGAGCAAGCAACAAAGCAG 769

QY 5222 ACCCATCTCTATAAACTAAATAATAGTTGGCATGTTGGCATGCTGGCATGCTGCTAGTCC 5281  
Db 768 ACCCGTCTCTATAAACTAAATAATAGTTGGCATGTTGGCATGCTGCTAGTCC 709

QY 5282 CAGTACTCCAGAGCGTGGATGGATCA---TCTGAGCCTCAGGAGTTGAGCTGCTGCT 5338  
Db 708 TAGCTACTAGGAGCGTGGAGGAGAGATCGTTGAACCCCGGAGAGCGAGGTTCCAGT 649

QY 5339 GAGCTGTGACTGCGCACTGCTCAGTGGCACTGCTGGCAACAGCAAGCAAGCCCTGCTTAA 5398  
Db 648 GAGTTGAGATTGTGCGCACTGCTCAGTGGCACTGCTGGCAACAGCAAGCAAGCCCTGCTTAA 590

QY 5399 AAAAAAGAAAAA 5414  
Db 589 AAAAAAGAAAAA 574

RESULT 10  
US-09-016-434-1449/c

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; Sequence 1449, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1449:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4079 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: q727358
; US-09-016-434-1449

Query Match 3.2%; Score 177.2; DB 4; Length 4079;
Best Local Similarity 74.5%; Pred. No. 2.3e-34;
Matches 237; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY 5102 AAATTCTAAGAAGAGCTGGGTGAGTGGCTCACACCTTTAATCCAGCACTTTGGGAAG 5161
DB 1786 AAAACATGATGATTGGCGGGTGGTGTTCACACCTGTATCTCAGTACTTTGGGAGG 1727
QY 5162 CAAGCGAAGAGACTGCTTGAACAGAGAGTTTGAGACAGCCTGAGCAACAAAGCAAG 5221
DB 1726 CCAAGCGAGATGGATCAGATGAACCCAGGAGTTCAAGACCAAGCCTGGGCAACATGGTAA 1667
QY 5222 ACCCATCTCTATAAAATCTAAAAATTTAGTTGGGATGGTGGACATGCTGTAGTCC 5281
DB 1666 ATCCTGTCTTTACAAAATACAAAATTTAGTGGCATGGTGTGATACCTGTGTCC 1607
QY 5282 CAGCTACTCCAGAGCTGAGATG---GATCATCTGAGCCTCAGGAGTTGAGGCTGAGT 5338
DB 1606 CAGCAACTCGAGAGCTGAGTGGGAGAAATCGTTAAGCCTGGAAGGTGAGGCTGCAGC 1547
QY 5339 GAGCTGTGACTGGCAGCTGCACTCCAGTCTGGGACAAACAGCAACACCTGCTTTAAA 5398
DB 1546 GAGCTAATGATTGTGCAGCTGCATCTCAGTCTGGGCCGCGAGCTGACAGCCCTGCTCAAC 1487
QY 5399 AAAAAAAGAAAAAAA 5416
DB 1486 AACACAAACAAACAAA 1469
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RESULT 11

US-09-580-1

; Sequence 1, Application US/09750580

; Patent No. 6455280

; GENERAL INFORMATION:

; APPLICANT: Yen, Frances

; APPLICANT: Denison, Blake

; APPLICANT: Bour, Barbara

; APPLICANT: Bihain, Bernard

; APPLICANT: Dumas Milne Edwards, Jean-Baptiste

; APPLICANT: Ducleit, Aymeric

; APPLICANT: Bougueleret, Lydia

; APPLICANT: Ebbets-Reed, Dana

; APPLICANT: Salter-Cid, Luisa

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH

; FILE REFERENCE: 89 US2.CIP

; CURRENT APPLICATION NUMBER: US/09/750,580

; CURRENT FILING DATE: 2000-12-28

; PRIOR APPLICATION NUMBER: US 09/599,362

; PRIOR FILING DATE: 2000-06-21

; PRIOR APPLICATION NUMBER: PCT/IB00/0101

; PRIOR FILING DATE: 2000-06-21

; PRIOR APPLICATION NUMBER: PCT/IB99/02058

; PRIOR FILING DATE: 1999-12-20

; PRIOR APPLICATION NUMBER: US 49/469/099

; PRIOR FILING DATE: 1999-12-21

; PRIOR APPLICATION NUMBER: US 60/113,686

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: US 60/141,032

; PRIOR FILING DATE: 1999-06-25

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: Patent.pm

; SEQ ID NO 1

; LENGTH: 81001

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc.feature

; LOCATION: 10946..12946

; OTHER INFORMATION: 5' regulatory region

; NAME/KEY: exon

; LOCATION: 12947..12958

; OTHER INFORMATION: exon 1

; NAME/KEY: exon

; LOCATION: 13470..13526

; OTHER INFORMATION: exon 2

; NAME/KEY: exon

; LOCATION: 13641..13752

; OTHER INFORMATION: exon 3

; NAME/KEY: exon

; LOCATION: 14271..15968

; OTHER INFORMATION: exon 4

; NAME/KEY: misc.feature

; LOCATION: 15969..17969

; OTHER INFORMATION: 3' regulatory region

; NAME/KEY: allele

; LOCATION: 1239

; OTHER INFORMATION: 20-828-311 : polymorphic base C or T

; NAME/KEY: allele

; LOCATION: 12347

; OTHER INFORMATION: 17-42-319 : polymorphic base C or T

; NAME/KEY: allele

; LOCATION: 15241

; OTHER INFORMATION: 17-41-250 : polymorphic base C or T

; NAME/KEY: allele

; LOCATION: 42218

; OTHER INFORMATION: 20-841-149 : polymorphic base A or G

; NAME/KEY: allele

; LOCATION: 45442

; OTHER INFORMATION: 20-842-115 : polymorphic base A or G

; NAME/KEY: allele

LOCATION: 77058  
OTHER INFORMATION: 20-853-415 : polymorphic base C or T  
NAME/KEY: primer\_bind  
LOCATION: 929..949  
OTHER INFORMATION: 20-828.pu  
NAME/KEY: primer\_bind  
LOCATION: 1357..1377  
OTHER INFORMATION: 20-828.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 12029..12050  
OTHER INFORMATION: 17-42.pu  
NAME/KEY: primer\_bind  
LOCATION: 12581..12603  
OTHER INFORMATION: 17-42.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 14992..15012  
OTHER INFORMATION: 17-41.pu  
NAME/KEY: primer\_bind  
LOCATION: 15460..15482  
OTHER INFORMATION: 17-41.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 42070..42090  
OTHER INFORMATION: 20-841.pu  
NAME/KEY: primer\_bind  
LOCATION: 42572..42591  
OTHER INFORMATION: 20-841.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 45328..45347  
OTHER INFORMATION: 20-842.pu  
NAME/KEY: primer\_bind  
LOCATION: 45863..45883  
OTHER INFORMATION: 20-842.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 76644..76664  
OTHER INFORMATION: 20-853.pu  
NAME/KEY: primer\_bind  
LOCATION: 77166..77185  
OTHER INFORMATION: 20-853.rp complement  
NAME/KEY: primer\_bind  
LOCATION: 1220..1238  
OTHER INFORMATION: 20-828-311.mis  
NAME/KEY: primer\_bind  
LOCATION: 12346  
OTHER INFORMATION: 17-42-319.mis  
NAME/KEY: primer\_bind  
LOCATION: 12348..12366  
OTHER INFORMATION: 17-42-319.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 15222..15240  
OTHER INFORMATION: 17-41-250.mis  
NAME/KEY: primer\_bind  
LOCATION: 15242..15260  
OTHER INFORMATION: 17-41-250.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 42199..42217  
OTHER INFORMATION: 20-841-149.mis  
NAME/KEY: primer\_bind  
LOCATION: 42219..42237  
OTHER INFORMATION: 20-841-149.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 45423..45441  
OTHER INFORMATION: 20-842-115.mis  
NAME/KEY: primer\_bind  
LOCATION: 45443..45461  
OTHER INFORMATION: 20-842-115.mis complement  
NAME/KEY: primer\_bind  
LOCATION: 77039..77057  
OTHER INFORMATION: 20-853-415.mis  
NAME/KEY: primer\_bind  
LOCATION: 77059..77077

OTHER INFORMATION: 20-853-415.mis complement  
NAME/KEY: misc\_binding  
LOCATION: 1227..1251  
OTHER INFORMATION: 20-828-311.probe  
NAME/KEY: misc\_binding  
LOCATION: 12335..12359  
OTHER INFORMATION: 17-42-319.probe  
NAME/KEY: misc\_binding  
LOCATION: 15229..15253  
OTHER INFORMATION: 17-41-250.probe  
NAME/KEY: misc\_binding  
LOCATION: 42206..42230  
OTHER INFORMATION: 20-841-149.probe  
NAME/KEY: misc\_binding  
LOCATION: 45430..45454  
OTHER INFORMATION: 20-842-115.probe  
NAME/KEY: misc\_binding  
LOCATION: 77046..77070  
OTHER INFORMATION: 20-853-415.probe  
US-09-750-580-1  
Query Match 3.2%; Score 176.8; DB 4; Length 81001;  
Best Local Similarity 77.2%; Pred. No. 1.7e-33;  
Matches 241; Conservative 0; Mismatches 67; Indels 4; Gaps 2;  
QY 5098 AATTAAATTTCTAAGAGAGAGCTGGGTGCAGTGGCTCACACCTTTTAAATCCACGACTTTGG 5157  
Db 69814 AATTAAAGAGAAAGTGTGGCTGGGGGCGAGTGGCTCATGTCATGTCATGCTTTGG 69873  
QY 5158 GAAGCCAAGCGAGAGAGACTGCTTTGAAACAGGAGTTTGAGACCCAGCTTGAGCAACAAG 5217  
Db 69874 GAGCTGAGGTGGGTAGTTGCTTGGAGCCCGAGAGTTTGAGACCCAGCTTGAGCAACAAG 69933  
QY 5218 CAAGACCCCATCTCTATAAAACCTAAAAAAATTTAGTTGGGCATGGTGGCAGCATGCTGTA 5277  
Db 69934 TGAGACCTTGTCTTACATAAGTTTAAAAAATTAGTGGCATGGTGGCAGCCACCTGTA 69993  
QY 5278 GTCCAGCTACTCCAGAGGCTGAGTGA---TCATCTGAGCCTCAGGAGTTGAGGCTG 5334  
Db 69994 GCCCAGCTACTTGAGAGGCTGAGTGGGAGGATCACTTGAAGTCTGGGAGTTGAGGCTG 70053  
QY 5335 CAGTGAGCTGTGACTGGCCACTCCAGTCTGGGACACAGAGAGACCCCTGCTCT 5394  
Db 70054 CAGTGAGCTGTGATTGAGCCACTGCCTCCAGCCAGGG-TGACAGAGTAAGACTCTGCT 70112  
QY 5395 TAAAAAATAAAAA 5406  
Db 70113 CAAAAAATAAAAA 70124  
RESULT 12  
US-08-480-784-20/c  
Sequence 20, Application US/08480784  
Patent No. 5693473  
GENERAL INFORMATION:  
APPLICANT: Skolnick, Mark H.  
APPLICANT: Goldgar, David E.  
APPLICANT: Miki, Yoshio  
APPLICANT: Swenson, Jeff  
APPLICANT: Kamb, Alexander  
APPLICANT: Harshman, Keith D.  
APPLICANT: Shattuck-Bidens, Donna M.  
APPLICANT: Tavtigian, Sean V.  
APPLICANT: Wiseman, Roger W.  
APPLICANT: Futreal, P. Andrew  
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer  
TITLE OF INVENTION: Susceptibility Gene  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC

COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 FILING DATE: US/08/480,784  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/409,305  
 FILING DATE: 24-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/348,824  
 FILING DATE: 29-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/308,104  
 FILING DATE: 16-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/289,221  
 FILING DATE: 12-AUG-1994  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24884-109347  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6769 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-08-480-784-20

Query Match 3.2%; Score 176.2; DB 1; Length 6769;  
 Best Local Similarity 75.9%; Pred. No. 5.5e-34;  
 Matches 245; Conservative 0; Mismatches 73; Indels 5; Gaps 2;

QY 5098 AATTAAATCTAAGAGAGGCTGGTGCAGTGCACACCTTTATCCAGCACTTTGG 5157  
 DB 6559 AATTAAGTAAAGGCGAGGCGACGATGCTCAAGCTGTACTGCACACTTTGG 6500  
 QY 5158 GAAGCCAAAGGAGGAGGAGCTCTTTAAACACGAGGATTTGAGACCGCTTGACCAAAAG 5217  
 DB 6499 GAGGCTGAAGTGGGAGAGCTCTTTAGTCCAGGAGTTTGAACAGCCTCGGTAAACATGG 6440  
 QY 5218 CAGACCCCATCTCTATAAACTTAAATAATAGTTGGCATGTGGCAGCATGCTCTGTA 5277  
 DB 6439 TGAACCCCATCTCTATAAACCAAAATTAACCGGTGTGGTGGCATCGGCTCTGTA 6380  
 QY 5278 GTCCAGCTACTCCAGGCTGTA----GATGGATCATCTGAGCCTCAGAGGTTTGAGCCT 5333  
 DB 6379 GTCCAGCTACTCAGAGGCTGAAGTGGAGGATAGCTTGGAGCCTTTGGAGGTGAGGTT 6320  
 QY 5334 GAGTGAAGCTGTGACTGCGCCACTGCATCCAGTCTGGGACACAGCAACACCTCTGC 5393  
 DB 6319 GAGTGAAGCAAGATTGATCACTGCACTCAGCCTGGG-CAACAGAGTGAGACCCCATC 6261  
 QY 5394 TTAATAAAAAAAAAAAAAAAAAAAAA 5416  
 DB 6260 TCAAAAAAAAAAACAACAACAAA 6238

RESULT 13  
 US-08-483-553-20/c  
 Sequence 20, Application US/08483553  
 Patent No. 5709999  
 GENERAL INFORMATION:  
 APPLICANT: Skolnick, Mark H.  
 APPLICANT: Goldgar, David E.  
 APPLICANT: Miki, Yoshio  
 APPLICANT: Swenson, Jeff  
 APPLICANT: Kamb, Alexander  
 APPLICANT: Harshman, Keith D.  
 APPLICANT: Shattuck-Eidens, Donna M.  
 APPLICANT: Tavtigian, Sean W.  
 APPLICANT: Wiseman, Roger W.  
 APPLICANT: Futreal, P. Andrew  
 TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer  
 NUMBER OF SEQUENCES: 85  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/483,553  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/409,305  
 FILING DATE: 24-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/348,824  
 FILING DATE: 29-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/308,104  
 FILING DATE: 16-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/289,221  
 FILING DATE: 12-AUG-1994  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24884-109347  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6769 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-08-483-553-20

Query Match 3.2%; Score 176.2; DB 1; Length 6769;  
 Best Local Similarity 75.9%; Pred. No. 5.5e-34;  
 Matches 245; Conservative 0; Mismatches 73; Indels 5; Gaps 2;

QY 5098 AATTAAATCTAAGAGAGGCTGGTGCAGTGCACACCTTTATCCAGCACTTTGG 5157  
 DB 6559 AATTAAGTAAAGGCGAGGCGACGATGCTCAAGCTGTACTGCACACTTTGG 6500  
 QY 5158 GAAGCCAAAGGAGGAGGAGCTCTTTAAACACGAGGATTTGAGACCGCTTGACCAAAAG 5217  
 DB 6499 GAGGCTGAAGTGGGAGAGCTCTTTAGTCCAGGAGTTTGAACAGCCTCGGTAAACATGG 6440  
 QY 5218 CAGACCCCATCTCTATAAACTTAAATAATAGTTGGCATGTGGCAGCATGCTCTGTA 5277  
 DB 6439 TGAACCCCATCTCTATAAACCAAAATTAACCGGTGTGGTGGCATCGGCTCTGTA 6380  
 QY 5278 GTCCAGCTACTCCAGGCTGTA----GATGGATCATCTGAGCCTCAGAGGTTTGAGCCT 5333  
 DB 6379 GTCCAGCTACTCAGAGGCTGAAGTGGAGGATAGCTTGGAGCCTTTGGAGGTGAGGTT 6320  
 QY 5334 GAGTGAAGCTGTGACTGCGCCACTGCATCCAGTCTGGGACACAGCAACACCTCTGC 5393  
 DB 6319 GAGTGAAGCAAGATTGATCACTGCACTCAGCCTGGG-CAACAGAGTGAGACCCCATC 6261  
 QY 5394 TTAATAAAAAAAAAAAAAAAAAAAAA 5416  
 DB 6260 TCAAAAAAAAAAACAACAACAAA 6238



MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,554B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/409,305  
FILING DATE: 24-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,824  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,104  
FILING DATE: 16-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,266  
FILING DATE: 02-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,221  
FILING DATE: 12-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109347  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6769 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
US-08-483-554B-20

Query Match	3.2%	Score 176.2	DB 1	Length 6769	
Best Local Similarity	75.9%	Pred. No. 5.5e-34			
Matches 245	Conservative	0	Mismatches 73	Indels 5	Gaps 2
QY	5098	AATTAAATTTCTAAGAGAGCTGGGTGCAGTGGCTCAGACCTTTTAAATCCAGACACTTTGG	5157		
DB	6559	AATTAAAGTAAGAGGGCAGGCCAGGCACAGTGGCTCAAGCCTGTAACTGACGACCTTTGG	6500		
QY	5158	GAAGCCCAAGGCAGGAACACTGCTTTGAAAACAGAGAGTTTGACACAGACCTGAGCAACAAG	5217		
DB	6439	GAGGCTGAAGTGGCGACACTGCTTGTAGTCCAGAGAGTTTGAGCCAGACCTCGGTAACTGG	6440		
QY	5218	CAAGACCCCATCTCTATAAAAACTAAAAAAATTTAGTTGGGCATGTTGGCACATGCCCTGTA	5277		
DB	6439	TGAACCCCATCTCTATAAAACACAAAAAATTAACCGGGTGTGGTGGCATGCOCCTGTGA	6380		
QY	5278	GTCCACAGTACTCCAGAGGGCTGA --- GATGGATCATCTGAGCCTCAGAGGTTGAGCCT	5333		
DB	6379	GTCCACAGTACTCCAGAGGGCTGAAGTGGGAGATAGCTTTGAGCCTTTGGAGGTGGAGTT	6320		
QY	5334	CGAGTGAGCTGTGACTCGGCCCATGTGCATCTCCAGTCTTGGGCAACAACAGACAGACCCCTGTC	5393		
DB	6319	CGAGTGAGCCCAAGATTGCAATCATCTGCATCTCCAGCCTGGG - CAACAGAGTGAGACCCCATC	6261		
QY	5394	TTAAAAAAGAAAAAAGAAAAA 5416			
DB	6260	TCAAAAAAGAAAAAACAACAAACAAA 6238			

Search completed: March 21, 2004, 22:18:51

Result No.	Score	Query Match	Length	DB	ID	Description
1	5525	100.0	5525	9	US-09-515-806-1	Sequence 1, Appl
2	5217.8	94.4	5305	15	US-10-258-106-33	Sequence 33, Appl
3	5040.8	91.2	5044	12	US-10-112-944-117	Sequence 117, App
4	5005.2	90.6	5094	12	US-10-174-333-138	Sequence 138, App
5	4733	85.7	4989	10	US-09-842-758-3	Sequence 3, Appl
6	4733	85.7	4989	12	US-10-174-333-3	Sequence 3, Appl
7	4462.4	80.8	4861	12	US-10-112-944-90	Sequence 90, Appl
8	4436.4	80.3	4346	12	US-10-425-114-2618	Sequence 2618, A
9	2928.8	53.0	2936	9	US-09-836-332-6	Sequence 6, Appl
10	2144.6	38.8	2200	9	US-09-925-301-184	Sequence 184, App
11	1716.4	31.1	1845	14	US-10-006-285-498	Sequence 498, App
12	886.8	16.1	897	14	US-10-204-887-29	Sequence 29, Appl
13	517.4	9.4	519	9	US-09-998-598-753	Sequence 753, App
14	373.4	6.8	471	14	US-10-006-285-340	Sequence 340, App
15	368.4	6.7	691	15	US-10-062-674-1525	Sequence 1525, AP

	Query Match	100.0%;	Score 5525;	DB 9;	Length 5525;
	Best Local Similarity	100.0%;	Pred. No. 0;		
	Matches 5525;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	TCGCCCCACGCGTTCGCACACGCGCCCGCCAGCAGAGCGCGCCCTGCCCTTGGCGCGAGCGCTG	60		
Db	1	TCGCCCCACGCGTTCGCACACGCGCCCGCCAGCAGAGCGCGCCCTGCCCTTGGCGCGAGCGCTG	60		
QY	61	CCATGGCTTGGGGGCGCGTGGGGGCGCGCCCGGGCGCGGACGAGCCTCGGAGAGGTACC	120		
Db	61	CCATGGCTTGGGGGCGCGTGGGGGCGCGCCCGGGCGCGGACGAGCCTCGGAGAGGTACC	120		
QY	121	CGCAACGACGAGACCCAGAGCTACAGGCCCTTGGAGGCCATCTACGGCGCGGATTTCCAAG	180		
Db	121	CGCAACGACGAGACCCAGAGCTACAGGCCCTTGGAGGCCATCTACGGCGCGGATTTCCAAG	180		



QY 181 ACCTGCGCGGACGCTTGGGACCGGTCAAGAGCCCTCGAAATCAATTTAGTTTGT 240  
DB 181 ACCTGCGCGGACGCTTGGGACCGGTCAAGAGCCCTCGAAATCAATTTAGTTTGT 240  
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DB 241 ACCCTCAAGGCTTAACCTGGTGAAGAGTATATGTAAAGTGGATTTGAGGTTAAATGCC 300  
QY 301 CACCTACCTATCCAGATGTAGTTCCTCGAAATAGAGTTTAAATAATGCAAGGTCTATCAA 360  
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QY 361 ATGAAGTGTCAATTTGTTAAATCTCGCTAGAGAACTGGCCAGAAACACTGTGGGG 420  
DB 361 ATGAAGTGTCAATTTGTTAAATCTCGCTAGAGAACTGGCCAGAAACACTGTGGGG 420  
QY 421 AGGTGATGATCTTTGAACTGGCTTACCACTGTGAGTCAATTTCTCAGCGAGCATAAACAAGC 480  
DB 421 AGGTGATGATCTTTGAACTGGCTTACCACTGTGAGTCAATTTCTCAGCGAGCATAAACAAGC 480  
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QY 601 AGAGAAGAAAGAGAGATAAAGAGAGAGAAAGAAAGAAAGAAATGGCTAAGCAGGAAC 660  
DB 601 AGAGAAGAAAGAGAGATAAAGAGAGAGAAAGAAAGAAAGAAATGGCTAAGCAGGAAC 660  
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DB 721 ACAGAACCGCTGCCATCTCATAGAGGCTCTCTGACTTTGTAGGAAATGGTAAACATC 780  
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DB 781 GGGCAAACTCTCAGGAGGCTTAGGCGAGAACTGCTAGTATTTCTGTATGTAAATGAG 840  
QY 841 ATCTCTCGGCTCTGTGAAATCTGTATTTCAATATGCGGAGTCTCTGATCAGCTCATGG 900  
DB 841 ATCTCTCGGCTCTGTGAAATCTGTATTTCAATATGCGGAGTCTCTGATCAGCTCATGG 900  
QY 901 TGCAAAAAGGGAATGTATTGGCAGTGTGAACAACTTGGAAATTTAGTCTACATGCTT 960  
DB 901 TGCAAAAAGGGAATGTATTGGCAGTGTGAACAACTTGGAAATTTAGTCTACATGCTT 960  
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DB 1021 AATGGGTCCATCTCTTACAGTCAAGAAAGAGAGAGATGTAAAGTCAAAAGACAGA 1080  
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DB 1081 TTTCAAGGAACAGAAACAGAAATTTCAACTCACTGTGTAATAATGAGCCATCCCAATGTAGTAC 1140  
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DB 1141 GCTACCTTGCAATGAATCTCAAGAGGAGAGAGAGTCTGCTGGTGGGACATTTTAGTGG 1200  
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DB 1201 AGCACAATTAGTGGGTCTCTTGTGTCACACCTCGAGCCACTCAGGCCCCCATCCCTGTGC 1260  
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QY 1801 AGAGACAGTTTTCCTGATCTTCTTATGAGTGTGAAGATTAACAATCTCTGTAAGGAG 1860  
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## RESULT 2

US-10-258-106-33

; Sequence 33, Application US/10258106

; Publication No. US20040018185A1

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1  ; GENERAL INFORMATION:
2  ; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
3  ; APPLICANT: GANDHI, Ameena R.; TRIBOULSY, Catherine M.
4  ; APPLICANT: KEARNEY, Liam; GRIFFIN, Jennifer A.
5  ; APPLICANT: NGUYEN, Daniel B.; BANDMAN, Olga
6  ; APPLICANT: LU, Dyung Aina M.; LAL, Preeti G.
7  ; APPLICANT: BURFORD, Neil; KHAN, Farrah A.
8  ; APPLICANT: WALIA, Narinder K.; YAO, Monique G.
9  ; APPLICANT: PATTERSON, Chandra; BURRILL, John D.
10 ; APPLICANT: MARCUS, Gregory A.; ZINGLER, Kurt A.
11 ; APPLICANT: RECIPON, Shirley A.; LU, Yan
12 ; APPLICANT: POLICKY, Jennifer L.; THORNTON, Michael B.
13 ; APPLICANT: TANG, Y. Tom; HAPFALIA, April J.A.
14 ; APPLICANT: ELLIOTT, Vicki S.; BAUGHN, Mariah R.
15 ; APPLICANT: WALSH, Roderick T.; RAMKUMAR, Javalakmi
16 ; APPLICANT: BOROWSKY, Mark L.; AU-YOUNG, Janice K.
17 ; APPLICANT: HILLMAN, Jennifer L.; GURURAJAN, Rajagopal
18 ; TITLE OF INVENTION: HUMAN KINASES
19 ; FILE REFERENCE: PI-0076 USN
20 ; CURRENT APPLICATION NUMBER: US/10/258,106
21 ; CURRENT FILING DATE: 2002-10-18
22 ; PRIOR APPLICATION NUMBER: PCT/US01/12992
23 ; PRIOR FILING DATE: 2001-04-20
24 ; PRIOR APPLICATION NUMBER: US 60/199,021
25 ; PRIOR FILING DATE: 2000-04-20
26 ; PRIOR APPLICATION NUMBER: US 60/200,226
27 ; PRIOR FILING DATE: 2000-04-28
28 ; PRIOR APPLICATION NUMBER: US 60/202,339
29 ; PRIOR FILING DATE: 2000-05-05
30 ; PRIOR APPLICATION NUMBER: US 60/203,505
31 ; PRIOR FILING DATE: 2000-05-11
32 ; PRIOR APPLICATION NUMBER: US 60/205,654
33 ; PRIOR FILING DATE: 2000-05-18
34 ; PRIOR APPLICATION NUMBER: US 60/207,739
35 ; PRIOR FILING DATE: 2000-05-26
36 ; PRIOR APPLICATION NUMBER: US 60/208,795
37 ; PRIOR FILING DATE: 2000-06-01
38 ; NUMBER OF SEQ ID NOS: 36
39 ; SOFTWARE: PERL Program
40 ; SEQ ID NO 33
41 ; LENGTH: 5305
42 ; TYPE: DNA
43 ; ORGANISM: Homo sapiens
44 ; FEATURE:
45 ; NAME/KEY: misc_feature
46 ; OTHER INFORMATION: Incyte ID No. US20040018185A1 7474
47 ; US-10-258-106-33

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	Query Match	94.4%;	Score 5217.8;	DB 15;	Length 5305;	
	Best Local Similarity	99.5%;	Pred. No. 0;			
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US-10-174-333-138
; Sequence 138, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zerkhusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchervnev, Velizar T.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grosse, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsbrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10174,333
; CURRENT FILING DATE: 2002-05-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
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; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: CuroSeqList version 0.1
; SEQ ID NO 138
; LENGTH: 5094
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20)...(4897)
US-10-174-333-138
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Query Match      90.6%; Score 5005.2; DB 12; Length 5094;
Best Local Similarity 98.6%; Pred. No. 0;
Matches 5086; Conservative 3; Indels 69; Gaps 1;
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DB 6 GCGGAGCGCTCCATGGCTGGGGCCCTGGGGCCCCCGGGCGGGCGGGAGCGCCCTC 65
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DB 666 ACCCAGGAGCAGACAGACGGCTGCTTCTACATGAGGCTCTCTGACTTTGTAGGAA 725
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DB 726 ATGTAAACATCGGGCAAACTCCTCAGGAAGGTCTAGGCGAGAACGTGATTTCTGTAT 785
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DB 786 GTAATAGTGAAGATTCTCTGGCTCTTGTGAATTCGTATTTCAATATGGGAGTCTCTG 845
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1309	TGCACACAAATCTGTGGTGCATTAAGGTCTAGTGCATCTAATGTCTTGGTGGATGCAG	1368	2389	ATTGCAATGAAGAAGTGGCTGCCATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG	2448
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1369	AAGGACCCGTCAAGATTACGGAATATAGCAATTTCTAAGCGCTTCGAGACATTTGCAAGG	1428	2449	ACTACCTATACATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAG	2508
1326	AAGGACCCGTCAAGATTACGGAATATAGCAATTTCTAAGCGCTTCGAGACATTTGCAAGG	1385	2406	ACTACCTATACATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAGATCCAG	2465
1429	AGGATGTTTGGAGCAACCCGAGTTCGTTTGTAGTGAACATGCTCTGCTTATAAAGCG	1488	2509	AGGACTGTATCGAGACACCGTTCAGACTCTGAGGCTTTTTCGAGAGATTCTGGATGAT	2568
1386	AGGATGTTTGGAGCAACCCGAGTTCGTTTGTAGTGAACATGCTCTGCTTATAAAGCG	1445	2466	AGGACTGTATCGAGACACCGTTCAGACTCTGAGGCTTTTTCGAGAGATTCTGGATGAT	2525
1489	GGAAGAAAGAGATGTTTGGCGCTTCGCGCTTCGCTGCTGCTCCCTCAGCCAGACAGG	1548	2569	TAGCTTATATCCATGAGAAAGGAATGATTCACCGGATTTGAAGCCTGTCAACATTTTTT	2628
1446	GGAAGAAAGAGATGTTTGGCGCTTCGCGCTTCGCTGCTGCTCCCTCAGCCAGACAGG	1505	2526	TAGCTTATATCCATGAGAAAGGAATGATTCACCGGATTTGAAGCCTGTCAACATTTTTT	2585
1549	AATGTGAGAGTACCTGTGACCAATCCCTAGTGAATTCAGAGTGAATTTCAAGATTTTC	1608	2629	TGATTTCTGATGACCATGTGAATATAGGTGATTTTGGTTCGCGACAGACCATCTAGCT	2688
1506	AATGTGAGAGTACCTGTGACCAATCCCTAGTGAATTCAGAGTGAATTTCAAGATTTTC	1565	2586	TGATTTCTGATGACCATGTGAATATAGGTGATTTTGGTTCGCGACAGACCATCTAGCT	2645
1609	TAAAGAAATGTGTGCTTGGATGACAAAGAAAGATGGAGTCCCGACAGTGTGTTGAAC	1668	2689	TTTCTGCTGACAGCAAAACAGAGATTCAGACAGGAGACTTGATTAAAGTCAGACCTTCAG	2748
1566	TAAAGAAATGTGTGCTTGGATGACAAAGAAAGATGGAGTCCCGACAGTGTGTTGAAC	1625	2646	TTTCTGCTGACAGCAAAACAGAGATTCAGACAGGAGACTTGATTAAAGTCAGACCTTCAG	2705
1669	ACAGCTTTATAAATCCCGACCAAAATGCTCTAGTGGAAACAAAGTCTGGAAGTTCTG	1728	2749	GTCACTTAACCTGGATGTTGGCACTGCTCTATGTAAGCCACAGGTCCTCAAGGAAGCA	2808
1626	ACAGCTTTATAAATCCCGACCAAAATGCTCTAGTGGAAACAAAGTCTGGAAGTTCTG	1685	2706	GTCACTTAACCTGGATGTTGGCACTGCTCTATGTAAGCCACAGGTCCTCAAGGAAGCA	2765
1729	GAGGACAGATTTAGTGAAGTGTATTCCTAGCAACCGGCTACCCAGTGTGCTGCTTCT	1788	2809	CCAAATCTGATACAAACAGAGTGGATCTCTTCAGCCCTGGGAATTTATCTTCTTTGAGA	2868
1686	GAGGACAGATTTAGTGAAGTGTATTCCTAGCAACCGGCTACCCAGTGTGCTGCTTCT	1745	2766	CCAAATCTGATACAAACAGAGTGGATCTCTTCAGCCCTGGGAATTTATCTTCTTTGAGA	2825
1789	TTAGTGAGACACAGAGACAGTTTCCCGATACCTTCAATGAGTTTGAAGATTTCAACTTC	1848	2869	TGCTCTATACCCCTGTCACGGCTTCAGAAAGATCTTGTTCACACCAACTCAGAG	2928
1746	TTAGTGAGACACAGAGACAGTTTCCCGATACCTTCAATGAGTTTGAAGATTTCAACTTC	1805	2826	TGCTCTATACCCCTGTCACGGCTTCAGAAAGATCTTGTTCACACCAACTCAGAG	2885
1849	TTGTTAAAGAGCTTTTGGAGCTGTCTCAAGTGCAGACAGATTTGGAGCTGTGCT	1908	2929	ATCCCACTTCGCTTAAGTTTCCAGAAAGACTTTCAGATGAGAGATGCAAAAGCAGAAAT	2988
1806	TTGTTAAAGAGCTTTTGGAGCTGTCTCAAGTGCAGACAAAGTTGGAGCTGTGCT	1865	2886	ATCCCACTTCGCTTAAGTTTCCAGAAAGACTTTCAGATGAGAGATGCAAAAGCAGAAAT	2945
1909	ACGAGTGAAGCGCATCCCCATCAACCGCGCCAGCGGCAAGTTCCGACGATCAAGGGCG	1968	2989	CAGTCATCTCTGGCTGTTGAACCAAGATCCAGCAAAACCGGCCACAGCCACAGAGCTGC	3048
1866	ACGAGTGAAGCGCATCCCCATCAACCGCGCCAGCGGCAAGTTCCGACGATCAAGGGCG	1925	2946	CAGTCATCTCTGGCTGTTGAACCAAGATCCAGCAAAACCGGCCACAGCCACAGAGCTGC	3005
1969	AAGTGACATCTGCTGACGGCTGACCATGAGAAACATTTGCGCTACTACAGCCCTGGA	2028	3049	TCAGAGTGAAGTGTGCTGCCCGCCACCCAGATGAGAGTTCAGAGTGTGATGAAGTGTGC	3108
1926	AAGTGACATCTGCTGACGGCTGACCATGAGAAACATTTGCGCTACTACAGCCCTGGA	1985	3006	TCAGAGTGAAGTGTGCTGCCCGCCACCCAGATGAGAGTTCAGAGTGTGATGAAGTGTGC	3065
2029	TCGAGCGGCACAGCGGCGCGGAGCGGGAGCGCGCCCGGACTCCGGGCCCTTGG	2088	3109	ACCAACGCTGACCAACGTTGGATGGAAAGGCTTACCGCACTTATGATGGCCAGATCTTCT	3168
1986	TCGAGCGGCACAGCGGCGCGGAGCGGGAGCGCGCCCGGACTCCGGGCCCTTGG	2045	3066	ACCAACGCTGACCAACGTTGGATGGAAAGGCTTACCGCACTTATGATGGCCAGATCTTCT	3125
2089	CCAAGGATGACCGAGCTGCACGCGGCGAGCGCGGAGCGGACACAGACGCGCTGGA	2148	3169	CGCAGCGATCTCCCTGCGCATCGATTACACTATGACAGCGACATCTGAGGGCAACT	3228
2046	CCAAGGATGACCGAGCTGCACGCGGCGAGCGCGGAGCGGACACAGACGCGCTGGA	2105	3126	CGCAGCGATCTCCCTGCGCATCGATTACACTATGACAGCGACATCTGAGGGCAACT	3185
2149	TAGAGCGCGCGCGCGGACCCATCTCAGCAGCTCGGTGGAGTGGAGCACTTCGGGCG	2208	3229	TCTCAATCCGTACAGCCAGATGACAGCATGTGTGTGAACCACTATCCGCACTTTTA	3288
2106	TAGAGCGCGCGCGCGGACCCATCTCAGCAGCTCGGTGGAGTGGAGCACTTCGGGCG	2165	3186	TCTCAATCCGTACAGCCAGATGACAGCATGTGTGTGAACCACTATCCGCACTTTTA	3245
2209	AGCGTCCGCGCAGTCCGTTTCCCGCCACCGCGCGGCTCAGCGATGACGAGGAG	2268	3289	ANAGACATGAGCTGTTCAGTTGTGTACTCTACTGCTTCCCGAAACAGACAAATAT	3348
2166	AGCGTCCGCGCAGTCCGTTTCCCGCCACCGCGCGGCTCAGCGATGACGAGGAG	2225	3246	ANAGACATGAGCTGTTCAGTTGTGTACTCTACTGCTTCCCGAAACAGACAAATAT	3305
2269	ACGACGAGACGAGTGGCTCTTCTCCAGTCTTCTGCTGCTTCAAGTTCTG	2328	3349	ATGACCAACAGAGCTGCGCTTATTCATGACACACAGCGGATGTGTGTGATGCTTCTT	3408
			3306	ATGACCAACAGAGCTGCGCTTATTCATGACACACAGCGGATGTGTGTGATGCTTCTT	3365

Qy	4489	GTGTGCTGGAGATGTAACCTGTGGACCACTGTACTGCGAAGAACTGAGCACTAAAGTCACTG	4544
Db	4446	GTGTGCTGGAGATGTAACCTGTGGACCACTGTACTGCGAAGAACTGAGCACTAAAGTCACTG	4505
Qy	4549	ATGAAGGAATGGCAGAGAAGCTTCGGATAATCTTGCAGTGCAGAAATCTTGAAGGGGTCAAT	4608
Db	4506	ATGAAGGAATGGCAGAGAAGCTTCGGATAATCTTGCAGTGCAGAAATCTTGAAGGGGTCAAT	4565
Qy	4609	TTTCTAATGCTTCAGGTTGTTTGAAATCCATGAGCAACAGTGGTTCCTCATTTGTGAGTG	4668
Db	4566	TTTCTAATGCTTCAGGTTGTTTGAAATCCATGAGCAACAGTGGTTCCTCATTTGTGAGTG	4625
Qy	4669	TGCTAGCCCGGAGAGAGCTGTGAGCCAGCACTAGGAGGCGCTATGAAACTACAGGTACAA	4728
Db	4626	TGCTAGCCCGGAGAGAGCTGTGAGCCAGCACTAGGAGGCGCTATGAAACTCTG-----	4678
Qy	4729	CTCGACTTCAGACCTCCCTTGGCAACTTATCATGAGAAAGCAGTGAATTTGAAATCTTGG	4788
Db	4679	-----	4678
Qy	4789	CTGTGGATCTACCCAGAAACAAATATTACAGTTTTTATCATTAGAGTGGAGTCTGTATG	4848
Db	4679	--GTGGATCTACCCAGAAACAAATATTACAGTTTTTATCATTAGAGTGGAGTCTGTATG	4736
Qy	4849	AACAGGCCATTTAACACAACCTGTGAAGCAGCTGCTGTACGCTGCCAAAGCAAGATACC	4908
Db	4737	AACAGGCCATTTAACACAACCTGTGAAGCAGCTGCTGTACGCTGCCAAAGCAAGATACC	4796
Qy	4909	TCAATTTAGTCTGTGTAAGAAATTTATAACATCAAGTAGTGAAGAAAGGTGCTGTGCTAT	4968
Db	4797	TCAATTTAGTCTGTGTAAGAAATTTATAACATCAAGTAGTGAAGAAAGGTGCTGTGCTAT	4856
Qy	4969	TTTCTGACAGCTATAGAGATGACTACTACAGAATCTTATTTTAAACCTTAAAGCAACTGTG	5028
Db	4857	TTTCTGACAGCTATAGAGATGACTACTACAGAATCTTATTTTAAACCTTAAAGCAACTGTG	4916
Qy	5029	TTAACTCATTTCAAACAGACAGAGGCTTATCTGGAATTAATGGAATGTTGTACATTCATC	5088
Db	4917	TTAACTCATTTCAAACAGACAGAGGCTTATCTGGAATTAATGGAATGTTGTACATTCATC	4976
Qy	5089	ATAATTTTAAATTTAAATTTCTTAAGAAAGAGCTGGGTGCAGTGGCTCACACCTTTAATCCCA	5148
Db	4977	ATAATTTTAAATTTAAATTTCTTAAGAAAGAGCTGGGTGCAGTGGCTCACACCTTTAATCCCA	5036
Qy	5149	GCATTTTGGGAAGCCAAGCAGGAAGACTGCTTTGAAACGAGGAGTTTGGAGCCAGCCT	5206
Db	5037	GCATTTTGGGAAGCCAAGCAGGAAGACTGCTTTGAAACGAGGAGTTTGGAGCCAGCCT	5094

Query Match	85.7%;	Score 4733;	DB 10;	Length 4989;
Best Local Similarity	98.4%;	Pred. No. 0;		
Matches 4911;	Conservative	0;	Mismatches 35;	Indels 47; Gaps 11;
Qy	63	ATGGCTGGGGCGCTGGGGCCCCCGGGCGGGCGGAGAGCTCCGAGAGCTACCGG	122	
Db	1	ATGGCTGGGGCGCTGGGGCCCCCGGGCGGGCGGAGAGCTCCGAGAGCTACCGG	60	
Qy	123	CAACGACAGGACCAAGGCTACAGCCCTGGAGGCCATCTACGGCGCGACCTTCCAGAC	182	
Db	61	CAACGACAGGACCAAGGCTACAGCCCTGGAGGCCATCTACGGCGCGACCTTCCAGAC	120	
Qy	183	CTGGCGCGGAGCGCTGGCGGACC-----GGTCAAGAGCCCCCTCAAAATCAATTAGTT	236	
Db	121	CTGGCGCGGAGCGCTGGCGGACGGTTAAGGTCAAGAGCCCCCTCAAAATCAATTAGTT	180	
Qy	237	TTGTACCCCTCAAGGCGCTAACTGGTGAAGAAGTATATGTAAGATGGATTGAGGGTAAA	296	
Db	181	TTGTACCCCTCAAGGCGCTAACTGGTGAAGAAGTATATGTAAGATGGATTGAGGGTAAA	240	
Qy	297	TGCCCACTTACCTATCCAGATGTAGTTCTCGAAATAGAGTTAAAAATGCCAAAGTCTA	356	
Db	241	TGCCCACTTACCTATCCAGATGTAGTTCTCGAAATAGAGTTAAAAATGCCAAAGTCTA	300	
Qy	357	TCAAAATGAAAGTGTCAATTTGTTAAAAATCTCGCCTAGAGAACTGGCCAGAGAAACACTGT	416	
Db	301	TCAAAATGAAAGTGTCAATTTGTTAAAAATCTCGCCTAGAGAACTGGCCAGAGAAACACTGT	360	
Qy	417	GGGGAG---GTGATGATCTTTGAACCTGGCTTACCACTGCGAGTCATTTCTCAGCGAGCAT	473	
Db	361	GGGGAGGTAGTATGATCATCTTTCAACTGGCTTACCACTGCGAGTCATTTCTCAGCGAGCAT	420	

1547 GGAATGTGGAGTACCCCTGTGACCATCCTAGTGACTTACAGCTGACTTTCAAGATT 1606  
1500 GGAATGTGGAGATGACCTGTGACCATCCTAGTGACTTACAGCTGACTTTCAAGATT 1559  
1607 TCTAAAGAA---ATGTGTGTGCTTGGATGACAAAGGAAGATGGAGTCCCCAGCAGTTGTT 1663  
1560 TCTAAAGAGAGATGTGTGTGCTTGGATGACAAAGGAAGATGGAGTCCCCAGCAGTTGTT 1619  
1564 GAAACACAGCTTTATTAATCCCGACGCAAAATGCTCTAGTGGAAACAAAGTCCCTGAA 1723  
1620 GAAACACAGCTTTATTAATCCCGACGCAAAATGCTCTAGTGGAAACAAAGTCCCTGAA 1677  
1724 TTTCTGGAGGCAAGATATGTTGAGACTGTTATTCCTAGCAACCCGGCTACCCAGTGTGC 1783  
1678 -TCTGAGGCAAGATATGTTGAGACTGTTATTCCTAGCAACCCGGCTACCCAGTGTGC 1736  
1784 CTTCTTTAGTGAGACACAGAGACAGTTTCCCGATCTTCAATGAGTTTGAAGATTACA 1843  
1737 CTTCTTTAGTGAGACACAGAGACAGTTTCCCGATCTTCAATGAGTTTGAAGATTACA 1796  
1844 ACTTCTTTGGTAAAGAGCTTTTGGAGCTGTCATCAAGGTGCAAGAACAAAGTTGGACGGCTG 1903  
1797 ACTTCTTTGGTAAAGAGCTTTTGGAGCTGTCATCAAGGTGCAAGAACAAAGTTGGACGGCTG 1856  
1904 CTGCTACGAGTGAAGCGCATCCCGATCAACCGCGGACCGCGAGTTCGGCAGGATCAA 1963  
1857 CTGCTACGAGTGAAGCGCATCCCGATCAACCGCGGACCGCGAGTTCGGCAGGATCAA 1916  
1964 GGGCGAAGTGACATGCTGTGTCACGGCTGCACCATGAGAACATGTGCGTACTACAAGC 2023  
1917 GGGCGAAGTGACATGCTGTGTCACGGCTGCACCATGAGAACATGTGCGTACTACAAGC 1976  
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2084 CTTGCGCAAGGATACCGAGCTGCAACCGCGGAGCGCGGAGCGCGGAGTTCGGCGGC 2143  
2037 CTTGCGCAAGGATGACCGAGCTGCAACCGCGGAGCGCGGAGCGCGGAGTTCGGCGGC 2096  
2144 CAGCGTAGAGCG 2203  
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2217 GGAACGACGAGGACGAGCAGCGTGGCGTCTTCTCCAGCTCGGTGGAGTGGAGCACTTC 2276  
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2277 TTCTGAAAGTGATATTATCTTTGACATGAAGATGAGAACAGTAAAGTCAAGATCAGGA 2336  
2384 TGAAGATTGCAATGAAAGAAATGGCTGCCATGAAAGTGAGCCATCACTGACGAGTGGGC 2443  
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2444 TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAGAGAGCACTTTACGAGACCAT 2503  
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2804 AAGACCAAACTGTGATACAAACAGAAAGTGGATCTCTTCAAGCTGGGAAATATCTTCT 2863  
2757 AAGACCAAACTGTGATACAAACAGAAAGTGGATCTCTTCAAGCTGGGAAATATCTTCT 2816  
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3044 ACTGCTCAAGAGTGAAGTCTGCTGCCCGCACCGAGATGGAGGAGTCAGAGCTGCATGAAGT 3103  
2997 ACTGCTCAAGAGTGAAGTCTGCTGCCCGCACCGAGATGGAGGAGTCAGAGCTGCATGAAGT 3056  
3104 GCTGCAACCAAGCTGACCAAGTGGAGGAGCTTACCGCAACCATGATGGGCCAGAT 3163  
3057 GCTGCAACCAAGCTGACCAAGTGGAGGAGCTTACCGCAACCATGATGGGCCAGAT 3116  
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3117 CTTCTGCAAGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3176  
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3284 CTTTAAAGACATGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3343  
3237 CTTTAAAGACATGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3296  
3344 AATATATGACCAACGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3403  
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3464 AAAACGATCTGCAATGAAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3523  
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3537 TGCTGAAATTTATCTACACTATCTATGAAATCATCCAGAGTTCGAGCACTTCAAGAAAG 3596  
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3597 AAATTTACAGTATTTTATTTGAAACCATCATCTGTTTAAAGCAATCTCTTACACTGTGG 3656  
3704 GATCCCAAGAGATAAATCAGTCAAGTCTACATTTCTCTATGCTGCTGACAGAGAA 3763

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3764 GCTGACGAGGAGAGAGTGAAGCTAAATTTGTAATCTGTCTTTGCTCTCTAAAGTCT 3823  
3717 GCTGACGAGGAGAGAGTGAAGCTAAATTTGTAATCTGTCTTTGCTCTCTAAAGTCT 3776  
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3777 GTGTGCGACTCTACAAAGTTTATGCAAGAGGAGATTTGCAAGATCTTATGCCAACAT 3836  
3884 AAATTCATTAATAAACAAGAAAACAGGTATGCAAGTTGGTGAAGTATGGCTTAAAGA 3943  
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3998 GATCAATTTGGGCTGTGTTTACAAGGTGACAGCAACAATGGAATCATCTTCAGTTTGT 4057  
3957 GATCAATTTGGGCTGTGTTTACAAGGTGACAGCAACAATGGAATCATCTTCAGTTTGT 4016  
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4077 TGACCTGCTGATTTCCCAAGTTTACAGGCGCCACAGCTCTGGGCGAGTTCCCACTGCCAT 4136  
4178 TGGGTGAGCTAGCTATAGACAGATATCTGCTGCTCTCAACATGAGGAA----- 4232  
4137 TGGGTGAGCTAGCTATAGACAGATATCTGCTGCTCTCAACATGAGGAACTGT 4196  
4233 ----TCTGTTCAATAAAGCTCTTGTGACCTCTGTTGTAAGTGTGGTCAAGTGTCTAT 4288  
4197 AGTTCTCTTACAATAGCTCTGGGACCTCTGTTGTAAGTGTGGGCGAGATGCTAT 4256  
4289 GTCCAGGCGCATCAACCTAACCCAGAACTCTGACAGCGGCATCACAGCAATCAT 4348  
4257 GTCCAGGCGCATCAACCTAACCCAGAACTCTGACAGCGGCATCACAGCAATCAT 4316  
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4317 GTACCACTGGTCAAGTTTCACTCCCAAGAGGAATTACAGAGTACTGACAGATCATGA 4376  
4403 AATCACTATGTGGCCCTTGTCTGATATAAAGAGGAGCCATGTCAGGTTAAGTCTTT 4462  
4377 AATCACTATGTGGCCCTTGTCTGATATAAAGAGGAGCCATGTCAGGTTAAGTCTTT 4436  
4463 CGAGAGGAGGAGGACAGAGAGCGGTGCTGAGACTGAACTTGTGACCATGTACT 4522  
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4583 TGCAGTGCAGAACTGAGGAGGCTATTTCTTAATGCTTCAGGTTGTTGAAATCCATGG 4642  
4557 TGCAGTGCAGAACTGAGGAGGCTATTTCTTAATGCTTCAGGTTGTTGAAATCCATGG 4616  
4643 AGCAACAGTGGTTCCCATTTGTGAGTGTGTAAGCCCGGAGAGGCTGTCAGCAGCACTAG 4702  
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4677 GAGGCGCTATGAACTCAGGTACAACTCGACTTCAGACCTCCCTTGGCACTTACATCA 4736  
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4737 GAAAGCAGTGAATTTGAAATTTGGCTGTAGTGAATCTACCAAGAAACAATATTACA 4796

RESULT 6

US-10-174-333-3  
; Sequence 3, Application US/10174333  
; Publication No. US20040029220A1  
; GENERAL INFORMATION:  
; APPLICANT: Vernet, Corine A.M.  
; APPLICANT: Fernandes, Elma R.  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Malyankar, Uriel M.  
; APPLICANT: Boldog, Ferenc L.  
; APPLICANT: Zerhusen, Bryan D.  
; APPLICANT: Spytek, Kimberly A.  
; APPLICANT: Majumder, Kumud  
; APPLICANT: Tchernev, Velizar T.  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Patturajan, Meera  
; APPLICANT: Burgess, Catherine E.  
; APPLICANT: Gangolli, Esha A.  
; APPLICANT: Smithson, Glenda  
; APPLICANT: Rastelli, Luca  
; APPLICANT: MacDougall, John R.  
; APPLICANT: Taupier, Raymond J.  
; APPLICANT: Grosse, William M.  
; APPLICANT: Szekeres, Edward S.  
; APPLICANT: Alsobrook, John P.  
; APPLICANT: Anderson, David W.  
; APPLICANT: Guo, Xiaojia (Sasha)  
; APPLICANT: Li, Li  
; APPLICANT: Zhong, Mei  
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
; FILE REFERENCE: 15966-783 CIP1  
; CURRENT APPLICATION NUMBER: US/10/174,333  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: 60/193,864  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 60/194,614  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: 60/195,063  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,066  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,067  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,068  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,069  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,070  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/195,510  
; PRIOR FILING DATE: 2000-04-06  
; PRIOR APPLICATION NUMBER: 60/219,855  
; PRIOR FILING DATE: 2000-07-21  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 186



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; SOFTWARE: CuraSeqList version 0.1
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; SEQ ID NO 3

; LENGTH: 4989

TYPE: DNA

ORGANISM: Homo sapiens

CREATION: HOME SUPPLIES  
; FEATURE:

; FEATURE:  
: NAME/KEY: CDS

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; NAME/KEY: CDS
: LOCATION: (1) (1986)

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; LOCATION: (TS-10-174-333-3)

Query Match 85.7%: Score 4733: DB 12: Length 4989:

Best Local Similarity 98.4%: Pred No. 0:

Desc Local Similarity 38.4%; Freq. NO: 0;  
 Matches 4911; Conservative 0; Mismatches 35; Indels 47; Gaps 11;

63	ATGCTGGGCGCGTGGGCGCCCGGCGCGCGCGGACGAGCCCTCGGAGAGCTACCCG	123
1	ATGGCTGGGCGCGTGGGCGCCCGGCGCGCGCGGACGAGCCCTCGGAGAGCTACCCG	60
123	CAAGACAGGACCAACGAGCTACAGGCGCTGGAGCCCATCTACGGCGCGAGCTTCCAAGAC	182
61	CAACGACAGGACCAACGAGCTACAGGCGCTGGAGCCCATCTACGGCGCGAGCTTCCAAGAC	120
183	CTGGCGCGGACGCTTCGGGACC-----GGTCAAGAGACCCCTCGAAATCAATTAGTT	236
121	CTGGCGCGGACGCTTCGGGACCGGTTAAGTCAAGAGCCCTCGAAATCAATTAGTT	180
237	TTGTACCCCTCAAGGCTAACTGTGTGAAGAGTATATGTAAAGTGGATTGAGGGTTAAA	296
181	TTGTACCCCTCAAGGCTAACTGTGTGAAGAGTATATGTAAAGTGGATTGAGGGTTAAA	240
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417	GGGGAG---GTGATGATCTTTGAACCTGGCTTACCACTGCAGTCAATTTCTCAGCGAGCAT	473
361	GGGGAGGTAGTGATGATCTTTGAACCTGGCTTACCACTGCAGTCAATTTCTCAGCGAGCAT	420
474	AACAAGCCCCCTCCCAAGTCTTTTTCATGAGAAATGCTGGAAAGCGGGCTCAGAGGAG	533
421	AACAAGCCCCCTCCCAAGTCTTTTTCATGAGAAATGCTGGAAAGCGGGCTCAGAGGAG	480
534	CAGCAGAGGCTGTTTGGAGGCCAAGCGGAAAGAGAGCAGGAGCAACGTGAAATCTCGCAT	593
481	CAACAGAGGCTGTTTGGAGGCCAAGCGGAAAGAGAGCAGGAGCAACGTGAAATCTCGCAT	540
594	GAGATTCTAGAGAGGAAGAGAGATATAAGAGAGAGAGAAAGAAAGAAAGAAATGCTTAAG	653
541	GAGATTCTAGAGAGGAAGAGAGATATAAGAGAGAGAGAAAGAAAGAAAGAAATGCTTAAG	600
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774	AAACATCGGGCAAACTCCTCAGGAAGTCT-----AGCGAGAACGTCAGTATTCTGTA	827
721	AAACATCGGGCAAACTCCTCAGGAAGTCTTAGGTTAAGCGAGAACGTCAGTATTCTGTA	780
828	TGTAATAGTGAAGATTCTCTGGCTCTTGTGAAATTTCTGTATTCAATATGGGAGTCTCT	887
781	TGTAATAGTGAAGATTCTCTGGCTCTTGTGAAATTTCTGTATTCAATATGGGAGTCTCT	840
888	GATAGCTCATGGTGCAAAAGGGAATGTATTGGCAGTGTAGAACAACTTGGAAAAATTA	947
841	GATAGCTCATGGTGCAAAAGGGAATGTATTGGCAGTGTAGAACAACTTGGAAAAATTA	900





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Db 4197 AAGTTCTGTTACAAATAGGCTCTGGGACCTCTCGTTGTTAAAGTGGTGGCGAGATGCTAT 4256
2Y 4289 GTCCAGGGCCATCAACCTAACCCAGAACTCTCGACAGAGGATCAGACAGCAAAATCAT 4348
Db 4257 GTCCAGGGCCATAAACCCTAACCCAGAACTCTCGACAGAGGATCAGACAGCAAAATCAT 4316
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Db 4317 GTACGACTGTGTCAGTTCAGTCCCAAGAGGAATTACAAGAGTACTGACAGACATCATGA 4376
2Y 4403 AATCACCTATGTGGCCCTTGTCTCGGATTAAGAGGAGCCATGTCAGGTTAAAGTCTTT 4462
Db 4377 AATCACCTATGTGGCCCTTGTCTCGGATTAAGAGGAGCCATGTCAGGTTAAAGTCTTT 4436
2Y 4463 CGAAGAGAAAGGACAGACAGAGAGCGTGTCTGGAGACTGAACCTTGTGGACCATGTACT 4522
Db 4437 CGAAGAGAAAGGACAGACAGAGAGCGTGTCTGGAGACTGAACCTTGTGGACCATGTACT 4496
2Y 4523 GCAGAACTGAGGCTAAAGTCACTGATGAAGGATGGCAGAGAGCTTCCGATAACT 4582
Db 4497 GCAGAACTGAGGCTAAAGTCACTGATGAAGGAAATTTTAGAGAGCTTCCGATAACT 4556
2Y 4583 TGCAGTGCANAATCTGAAGGGGTCAATTTCTAATGCTTTCAGGTTTGTGTTGAAATCCATGG 4642
Db 4557 TGCAGTGCANAATCTGAAGGGGTCAATTTCTAATGCTTTCAGGTTTGTGTTGAAATCCATGG 4616
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2Y 4763 GAAAGAGTGAATGAATTCCTGGCT---GTGGATCTACCCAAAGAAACAATATTACA 4819
Db 4737 GAAAGAGTGAATGAATTCCTGGCTGTAGTGGATCTACCCAAAGAAACAATATTACA 4796
2Y 4820 GTTTTATCATTTAGAGTGGGATGCTGATGAACAGGCATTTAAACAACTGTGAAGCAGCT 4879
Db 4797 GTTTTATCATTTAGAGTGGGATGCTGATGAACAGGCATTTAAACAACTGTGAAGCAGCT 4856
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Db 4857 GCTGTACGCTGCGCAAGCAAGAAATACCTCAAAATAGTCTGTGATGAATTTATTAACAT 4916
2Y 4940 CAAAGTAGAAAAGGAGTGTCTGTGCTATTCTGTACAGCTATAGAGTACTACTACAG 4999
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2Y 5000 AATCTATTATTA 5012
Db 4977 AATCTATTATTA 4989
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## RESULT 7

US-10-112-944-90

; Sequence 90, Application US/10112944

; Publication NO. US20040048249A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Yang, Yonghong

; APPLICANT: Wang, Gezhi

; APPLICANT: Zhang, Jie

; APPLICANT: Ren, Feiyang

; APPLICANT: Xue, Aidong J.

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Wehrman, Tom

; APPLICANT: Ghosh, Malabika

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; APPLICANT: Wang, Dunrui
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Zhiwei
; TITLE OF INVENTION: No. US20040048249A1el Nucleic Acids and
; TITLE OF INVENTION: Secreted Polypeptides
; FILE REFERENCE: 805A
; CURRENT APPLICATION NUMBER: US/10/112,944
; CURRENT FILING DATE: 2002-03-28
; PRIOR FILING DATE: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: US 09/519,705
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 09/552,929
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 924
; SOFTWARE: Pt_Fl_Genes Version 5.0
; SEQ ID NO 90
; LENGTH: 4861
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (364)..(4497)
; US-10-112-944-90
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## Query Match

80.8%; Score 4462.4; DB 12; Length 4861;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4474; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 715 GAGGACACAGAACGGTGGCCATTTCTACATGGAGGCTCTCCTGACCTTTGAGGAAATGGTA 774
Db 203 GAGGACACAGAACGGTGGCCATTTCTACATGGAGGCTCTCCTGACCTTTGAGGAAATGGTA 262
QY 775 AACATCGGGCAAACTCCTCTAGGAAGCTCTAGGGAGAACGTGATTTCTGTATTAATA 834
Db 263 AACATCGGGCAAACTCCTCTAGGAAGCTCTAGGGAGAACGTGATTTCTGTATTAATA 322
QY 835 GTGAAGATTTCTCTGGCTCTTGTGAAATTTCTGATTTCAATATGGGAGTCTCTGATCAGC 894
Db 323 GTGAAGATTTCTCTGGCTCTTGTGAAATTTCTGATTTCAATATGGGAGTCTCTGATCAGC 382
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Db 383 TCATGGTGCAAAAGGAAATGATTGGCAGTGATGAACAACTTGGAAATTAGTCTACA 442
QY 955 ATGCTTTGGAAACAGCCACTGGTGGCTTTGCTGTGTTGATGAGTGGTCTCTTCAGTGCC 1014
Db 443 ATGCTTTGGAAACAGCCACTGGTGGCTTTGCTGTGTTGATGAGTGGTCTCTTCAGTGCC 502
QY 1015 AGAAAAAATTTGGTCCATTTCCCTTACCAGTCAAGAAAAAGAGAGATTTGATAGTGC AAA 1074
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Db 563 AGCAGATTTCAAGGACAGAAACAGAAATTCACCTCCTGGTAAATTTGAGCCATCCAAATG 622
QY 1135 TAGTACGCTACCTTTGCAATGAATCTCAAGAGCAGACGACTCCATCGTGGTGGACATTT 1194
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Qy 1195 TAGTGGAGCACATTAGTGGGTCTCTCTGTGACACACCTGAGCACTCAGGCCCATCC 1254  
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Qy 2155 CGGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2214  
Db 1643 CGGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1702  
Qy 2215 CGGCCAGTGCCTGTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 2274  
Db 1703 CGGCCAGTGCCTGTTCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1762

Qy 2275 AGGACGAGCACGCTGGCGTCTTCTCCAGTCTCTTCTGCTCTCAGATTTCTGAAAGTG 2334  
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Qy 2395 ATGAAAAGATGGCTGCCATGAAAGTGAAGTGAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2454  
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Qy 2455 TATACATCCAGATGGAGTACTGTGAGAGAGCACTTTAGAGACCACTTGAAGCCAGGAC 2514  
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Db 2063 ATATCCATGAGAAAGGAATGATTCAACGGGATTTGAAGCTCTCAACATTTTTCGGATT 2122  
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Db 2123 TTGATGACCAATGTGAAATAGGTGATTTTGGTGGCGACAGACCACTTAGCCCTTTTCTG 2182  
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Db 2483 TCTCTGGCTGTTGAACGAGATCCAGAAAGCGGCCACAGCCACAGACTGCTCAAGA 2542  
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3775 GAGAGTGGAGCTTAAATTTGTAATCTGCTTTGTTCTTCTAATAGTCTGTGCACTCT 3834  
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4255 ACCTCCTGGTTGAAGTTGGTTCAGATGCTATGTCAGGGCCATCAACCTAACCCAGA 4314  
4315 AACTCTGACAGCAGGATCACAGCAAAATCATGTACGACTGTCACAGTCCCAAGAGG 4374  
4375 AATTACAAGAGTACTGACAGCATCATGAATACCTATGTGGCCCTGTCTCGGATAAG 4434  
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4495 TGGAGACTGAATCTTGTGACCATGTACTGACAGAACTGAGGACTAAAGTCACTGATGAA 4554  
3983 TGGAGACTGAATCTTGTGACCATGTACTGACAGAACTGAGGACTAAAGTCACTGATGAA 4042  
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4675 CCGCGAGAGAGCTGTGACGACACTAGGAGCGCTATGAAACTCAGGTACAAACTCGAC 4734  
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4523 TCATTTCAACAGCAGAGGCTTATCTGGAATTAAGAAATGTTGTACATTTCATCATTAAT 4582  
5095 TAAATTAATTTCTAAGAGAGGCTGGGTGACGTGG 5130  
4583 TAAATTAATTTCTAAGAGAGG-TGGGTGACGTGG 4617

RESULT 8  
US-10-425-114-26218  
; Sequence 26218, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaka, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 26218  
; LENGTH: 4438  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB4117-013-G9\_FU1  
US-10-425-114-26218

Query Match	80.3%;	Score	4436.4;	DB	12;	Length	4438;
Best Local Similarity	100.0%;	Pred. No.	0;				
Matches	4437;	Conservative	0;	Mismatches	1;	Indels	0;
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2b	1	CTTTGGAAACAGCCACTGGTGGCTTCTGCTGTTGATGAGTGGGTCCCTTCAGTGGCAGA	60				
2y	1018	AAAAAATGGGTCCATTCCTTACCAGTCAAGAAAAGAGAAAGATTGATTAAGTGCAAAAGC	1077				
2b	61	AAAAAATGGGTCCATTCCTTACCAGTCAAGAAAAGAGAAAGATTGATTAAGTGCAAAAGC	120				
2y	1078	AGATTCACAGGACAGAAACAGAAATCAACTCACTGGTAAATTTGAGCCATCCAAATGTAG	1137				
2b	1321	AGATTCACAGGACAGAAACAGAAATCAACTCACTGGTAAATTTGAGCCATCCAAATGTAG	180				
2y	1138	TACGCTACCTTGCATTAAGTAACTCAAGAGCAAGACGACTCCATCGTGGTGACATTTTAG	1197				
2b	181	TACGCTACCTTGCATTAAGTAACTCAAGAGCAAGACGACTCCATCGTGGTGACATTTTAG	240				
2y	1198	TGGAGCATTAGTGGGTCTCTCTGTCTGCACACCTTGAGCCACTCAGGCCCATCCCTG	1257				
2b	241	TGGAGCATTAGTGGGTCTCTCTGTCTGCACACCTTGAGCCACTCAGGCCCATCCCTG	300				
2y	1258	TCATCAGCTTCGCAGGTACACAGCTCAGCTCCCTGTCAGGCGCTTGATTATCTGCACAGCA	1317				
2b	301	TGCATCAGCTTCGCAGGTACACAGCTCAGCTCCCTGTCAGGCCCTTGATTATCTGCACAGCA	360				
2y	1318	ATTCTGTGGTGGAATGAAGTCCTGTAGTGCAATCTAATGCTTGTGGTGGATGGAAGGCACCG	1377				
2b	361	ATTCTGTGGTGGAATGAAGTCCTGTAGTGCAATCTAATGCTTGTGGTGGATGGAAGGCACCG	420				
2y	1378	TCAAGATTACGAGCTATAGCAATTTCTAAGCGCCCTCGACAGCATTTGCAAGAGGATGTGT	1437				
2b	421	TCAAGATTACGAGCTATAGCAATTTCTAAGCGCCCTCGACAGCATTTGCAAGAGGATGTGT	480				
2y	1438	TTGAGCAAAACCGAGTTCCTTTTATGTCGAATGCTCTGCCCTTATAAAACGGGGAAGAAG	1497				
2b	481	TTGAGCAAAACCGAGTTCCTTTTATGTCGAATGCTCTGCCCTTATAAAACGGGGAAGAAG	540				
2y	1498	GAGATGTTGGCGCTCTGGCCCTCTGCTGCTGCTCCCTCAGCCACAGGACAGGATGTGGAG	1557				
2b	541	GAGATGTTGGCGCTCTGGCCCTCTGCTGCTGCTCCCTCAGCCACAGGACAGGATGTGGAG	600				
2y	1558	AGTACCCCTGTGACACCTCCCTAGTGACTTTACCAGCTGACTTTTCAAGATTTTCTAAGAAAT	1617				
2b	601	AGTACCCCTGTGACACCTCCCTAGTGACTTTACCAGCTGACTTTTCAAGATTTTCTAAGAAAT	660				
2y	1618	GTGTGCTTGGATGACAAGGAAAGATGGAGTCCCAGCAGTTGTTGAAACACAGCTTTA	1677				
2b	661	GTGTGCTTGGATGACAAGGAAAGATGGAGTCCCAGCAGTTGTTGAAACACAGCTTTA	720				
2y	1678	TAAATCCCAGCAAAATAGCCTCTAGTGGAAACAAAGTCCTGAAGATTCTGGAGGACAAG	1737				
2b	721	TAAATCCCAGCAAAATAGCCTCTAGTGGAAACAAAGTCCTGAAGATTCTGGAGGACAAG	780				
2y	1738	ATTATGTTGAGACTGTATCTCTAGCAACCGGCTACCCAGTGTGCTCTTTTAGTGAGA	1797				
2b	781	ATTATGTTGAGACTGTATCTCTAGCAACCGGCTACCCAGTGTGCTCTTTTAGTGAGA	840				
2y	1798	CACAGAGACAGTTTTCCCGATCTTCAATTGAGTTTGAAGAAATTAACAATCTCTGGTAAAG	1857				
2b	841	CACAGAGACAGTTTTCCCGATCTTCAATTGAGTTTGAAGAAATTAACAATCTCTGGTAAAG	900				
2y	1858	GAGCTTTTGGAGCTGTCAATCAAGGTGCAGAAACAAGTTGGAAGCGCTGTGCTACGCAGTGA	1917				
2b	901	GAGCTTTTGGAGCTGTCAATCAAGGTGCAGAAACAAGTTGGAAGCGCTGTGCTACGCAGTGA	960				
2y	1918	AGCGCATCCCACTCAACCGCGCCAGCCGAGTTCGGCAGGATCAAGGGCGAAGTGACAC	1977				
2b	961	AGCGCATCCCACTCAACCGCGCCAGCCGAGTTCGGCAGGATCAAGGGCGAAGTGACAC	1020				
2y	1978	TGCTGTCAAGGCTGCACCATGAGAAATTTGTGCTGCTACTACAAACCCCTGGATCGAGCGGC	2037				

2101 AGTGTGCCCCCACCAGATGGAGGATGACAGTGCATGAAGTGTGTCGACACACGC 2160  
2118 TGACCAACGTGGATGGGAAGCCTACCGCACCATGATGCCAGATCTTCTCCGACGCA 3177  
2161 TGACCAACGTGGATGGGAAGCCTACCGCACCATGATGCCAGATCTTCTCCGACGCA 2220  
3178 TCTCCCTGCCATCGATACACCTATGACAGCAGACATCTGAGGGCACTTCTCAATCC 3237  
2221 TCTCCCTGCCATCGATACACCTATGACAGCAGACATCTGAGGGCACTTCTCAATCC 2280  
3238 GTACAGCCAAAGATCAGCAGCATGTGTGTAACCATCATCCGATCTTTAAAGACATG 3297  
2281 GTACAGCCAAAGATCAGCAGCATGTGTGTAACCATCATCCGATCTTTAAAGACATG 2340  
3298 GAGCTGTTCACTGTGTACTCCACTGCTTCCGGAACACACAAATATATGACACA 3357  
2341 GAGCTGTTCACTGTGTACTCCACTGCTTCCGGAACACACAAATATATGACACA 2400  
3358 ACGAGCTGCCCTATTATGAGCACACAGCGGATGTGTGATGCTTCCCTTTGACCTGC 3417  
2401 ACGAGCTGCCCTATTATGAGCACACAGCGGATGTGTGATGCTTCCCTTTGACCTGC 2460  
3418 GGATCCCTTTGGAAGATATGTGCAAGAAATATATATTGAATTTAAACGATCTGCA 3477  
2461 GGATCCCTTTGGAAGATATGTGCAAGAAATATATATTGAATTTAAACGATCTGCA 2520  
3478 TAGAAGCTGTGTTCAGGCGCGCAAGTTAGATCGATTTCAATCCCAAAGAACTTCTGGAGT 3537  
2521 TAGAAGCTGTGTTCAGGCGCGCAAGTTAGATCGATTTCAATCCCAAAGAACTTCTGGAGT 2580  
3538 GTGCATTTGATTTGATCTACTTACACCAACAGCTTCTGCCACATGCTGGAATTTATCT 3597  
2581 GTGCATTTGATTTGATCTACTTACACCAACAGCTTCTGCCACATGCTGGAATTTATCT 2640  
3598 ACACATATCTGAAATCATCAAGATTTCCAGACATTCAGGAAGAAATTAAGATATT 3657  
2641 ACACATATCTGAAATCATCAAGATTTCCAGACATTCAGGAAGAAATTAAGATATT 2700  
3658 ATTGAACCATACCATTTATGAAGCAATCTTACACTGTGGATCCCAAGAGATA 3717  
2701 ATTGAACCATACCATTTATGAAGCAATCTTACACTGTGGATCCCAAGAGATA 2760  
3718 AACTCAGTCAAGCTACATTTATCTGATGATGCTGTGACAGAACTGACAGGAGAG 3777  
2761 AACTCAGTCAAGCTACATTTATCTGATGATGCTGTGACAGAACTGACAGGAGAG 2820  
3778 AAGTGAAGCTAAATTTGTAATCTGCTTTGCTTTCTAATAGTCTGTGCTACTTACA 3837  
2821 AAGTGAAGCTAAATTTGTAATCTGCTTTGCTTTCTAATAGTCTGTGCTACTTACA 2880  
3838 AGTTTATGAACAGAGGAGATTTGCAAGATCTTATGCCAACAATTAATTCATTATTA 3897  
2881 AGTTTATGAACAGAGGAGATTTGCAAGATCTTATGCCAACAATTAATTCATTATTA 2940  
3898 AACAGAAAACAGGTATTTGACAGTGTGGTGAAGTATGGCTTAAAGACCTAGAGAGGTTG 3957  
2941 AACAGAAAACAGGTATTTGACAGTGTGGTGAAGTATGGCTTAAAGACCTAGAGAGGTTG 3000  
3958 TTGCACTGTTGAAGAACTCCGCATCAAGTTACAGGCTTCTGATCAATTTGGGCTTGGTTT 4017  
3001 TTGCACTGTTGAAGAACTCCGCATCAAGTTACAGGCTTCTGATCAATTTGGGCTTGGTTT 3060  
4018 ACAAGGTGACAGACAAATGGAATCATCTTCCAGTTTGTGGCTTTTCAATCAACGGAAGGC 4077  
3061 ACAAGGTGACAGACAAATGGAATCATCTTCCAGTTTGTGGCTTTTCAATCAACGGAAGGC 3120  
4078 AAGGGCTGTACTGAAATCTTCGAGCTGGAGGAGATATGACCTGCTGATTTCCCGAGT 4137  
3121 AAGGGCTGTACTGAAATCTTCGAGCTGGAGGAGATATGACCTGCTGATTTCCCGAGT 3180  
4138 TTAGAGGGCCACAAAGCTCTGGGGCCAGTTCCCACTGGCAATGGGGTCAGCATAGCTATAG 4197  
3181 TTAGAGGGCCACAAAGCTCTGGGGCCAGTTCCCACTGGCAATGGGGTCAGCATAGCTATAG 4240

4198 ACAAGATATCTCTGCTGCTCAACATGGAGGAATCTGTTACAAATAGCTCTTTGTGACC 4257  
3241 ACAAGATATCTCTGCTGCTCAACATGGAGGAATCTGTTACAAATAGCTCTTTGTGACC 3300  
4258 TCTGTTGTTAAGTGTGTTGTCAGATGTCTATGTCCAGGGCCATCAACCTAACCCAGAAAC 4317  
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4318 TCTGGACAGCGGCATCACAGCAGAAATCATGTACGACTGGTTCACAGTCCCAAGAGGAAT 4377  
3361 TCTGGACAGCGGCATCACAGCAGAAATCATGTACGACTGGTTCACAGTCCCAAGAGGAAT 3420  
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4438 GAAGCCATGTCAAGTTAAGTCTTTTCGAGAAGGAAGCAGACAGAGAGCGTGTGCTGG 4497  
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4498 AGACTGAATCTGTGGACCATGTACTGCAGAAACTGAGGACTAAAGTCACTGATGAAGGA 4557  
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4558 ATGSCAGAGAGCTTCCGATAATCTTGCAGTGCANAACTCTGAAGGGTCAATTTCTAATG 4617  
3601 ATGSCAGAGAGCTTCCGATAATCTTGCAGTGCANAACTCTGAAGGGTCAATTTCTAATG 3660  
4618 CTTTCAGGTTTGTGTAATCCATGAGCAACAGTGGTCCCATTTGTGAGTGTGCTAGGCC 4677  
3661 CTTTCAGGTTTGTGTAATCCATGAGCAACAGTGGTCCCATTTGTGAGTGTGCTAGGCC 3720  
4678 CGGAGAAGCTGTGAGCGACACTAGAGAGCGCTATGAAACTCAGGTACAAACTCGACTTC 4737  
3721 CGGAGAAGCTGTGAGCGACACTAGAGAGCGCTATGAAACTCAGGTACAAACTCGACTTC 3780  
4738 AGACTCCCTGTCACACTTACATCAGAAAGCAGTGAATTTGAAATTTCTGGGTGTGATC 4797  
3781 AGACTCCCTGTCACACTTACATCAGAAAGCAGTGAATTTGAAATTTCTGGGTGTGATC 3840  
4798 TACCAAAGAAACAATATACAGTTTATCATAGTGGGATGCTGATGAACAGGCAT 4857  
3841 TACCAAAGAAACAATATACAGTTTATCATAGTGGGATGCTGATGAACAGGCAT 3900  
4858 TTAACACAACTGTGAACAGCTGCTGACGCTGCAAGCAAGATACCTCAAAATTAG 4917  
3901 TTAACACAACTGTGAACAGCTGCTGACGCTGCAAGCAAGATACCTCAAAATTAG 3960  
4918 TCTGTGATGAAATTTATAACATCAAGTAGAAAAAAGGTGTCTGTGCTATTTCTGTACA 4977  
3961 TCTGTGATGAAATTTATAACATCAAGTAGAAAAAAGGTGTCTGTGCTATTTCTGTACA 4020  
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4021 GCTATAGAGATGACTACTACAGATCTTATTTTAAACCTTAAGAACTGCTGTTAACTCA 4080  
5038 TTTCAACACAGACAGAGGCTTACTTGGAAATTAATGGAATTTGTACATTCATTAATTTAA 5097  
4081 TTTCAACACAGACAGAGGCTTACTTGGAAATTAATGGAATTTGTACATTCATTAATTTAA 4140  
5098 AATTAAATTTTAAAGAGGCTGGGTGAGTGCACCTTTAATCCAGCAGCTTGG 5157  
4141 AATTAAATTTTAAAGAGGCTGGGTGAGTGCACCTTTAATCCAGCAGCTTGG 4200  
5158 GAAGCAAGGCGAGGAGACTGCTTTGAAACCCAGGAGTTTGAGACCAGGCTGAGCAACAAAG 5217  
4201 GAAGCAAGGCGAGGAGACTGCTTTGAAACCCAGGAGTTTGAGACCAGGCTGAGCAACAAAG 4260  
5218 CAAGACCCCTCTCTATAAAACTATAAAATTTAGTTGGGCATGGTGGCATGCCCTGTA 5277  
4261 CAAGACCCCTCTCTATAAAACTATAAAATTTAGTTGGGCATGGTGGCATGCCCTGTA 4320

QY 5278 GTCCAGCTACTCCAGAGGCTGAGATGGATCATCTGAGCCTCAGGAGGTTGAGGCTGCAG 5337  
Db 4321 GTCCAGCTACTCCAGAGGCTGAGATGGATCATCTGAGCCTCAGGAGGTTGAGGCTGCAG 4380  
QY 5338 TGAGCTGTGACTGCGCCACTGCACTCCAGCTCGGACCAAGAGCAAGACCCCTGTCTT 5395  
Db 4381 TGAGCTGTGACTGCGCCACTGCACTCCAGCTCGGACCAAGAGCAAGACCCCTGTCTT 4438

RESULT 9  
JS-09-836-392-6  
; Sequence 6, Application US/09836392  
; Patent No. US20020173458A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Protein Tyrosine Kinase Receptor Polynucleotides, Polypeptides, and Antibodies  
; FILE REFERENCE: PT020P1  
; CURRENT APPLICATION NUMBER: US/09/836,392  
; PRIOR FILING DATE: 2001-04-18  
; PRIOR APPLICATION NUMBER: PCT/US00/28066  
; PRIOR FILING DATE: 2000-10-11  
; PRIOR APPLICATION NUMBER: 60/159,542  
; PRIOR FILING DATE: 1999-10-15  
; PRIOR APPLICATION NUMBER: 60/165,914  
; PRIOR FILING DATE: 1999-11-17  
; PRIOR APPLICATION NUMBER: 60/189,027  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 6  
; LENGTH: 2946  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-836-392-6

Query Match 53.0%; Score 2928.8; DB 9; Length 2946;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2950; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2485 GCACCTTACGACACACCATTCACAGGAGCTGTATCGAGACACCGTCAGACTCTGGAGC 2544  
Db 12 GCACCTTACGACACACCATTCACAGGAGCTGTATCGAGACACCGTCAGACTCTGGAGC 71  
QY 2545 TTTTTCGAGAGATTCGGATGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGG 2604  
Db 72 TTTTTCGAGAGATTCGGATGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGG 131  
QY 2605 ATTTGAAGCTGTCAACATTTTGGATTCGTATGATGACCATGTGAAATAGGTGATTTTG 2664  
Db 132 ATTTGAAGCTGTCAACATTTTGGATTCGTATGATGACCATGTGAAATAGGTGATTTTG 191  
QY 2665 GTTTCGCGACACCATCTAGCCTTTCTGCTGACAGCAACAGACGATCAGACAGGAG 2724  
Db 192 GTTTCGCGACACCATCTAGCCTTTCTGCTGACAGCAACAGACGATCAGACAGGAG 251  
QY 2725 ACTTGATTAAGTCAGACCCCTTCAGTCACTTAACTGGGATGGTTGGCACTGCTCTCTATG 2784  
Db 252 ACTTGATTAAGTCAGACCCCTTCAGTCACTTAACTGGGATGGTTGGCACTGCTCTCTATG 311  
QY 2785 TAAAGCCAGAGGTCAGAGAGCACCACCAATCTGATACACCAAGAGTGGATCTCTTCA 2844  
Db 312 TAAAGCCAGAGGTCAGAGAGCACCACCAATCTGATACACCAAGAGTGGATCTCTTCA 371  
QY 2845 GCCTGGGAATATCTCTTTGAGATGTCCTATCACCCTAGGTCAACGGCTTCAGAAAGGA 2904  
Db 372 GCCTGGGAATATCTCTTTGAGATGTCCTATCACCCTAGGTCAACGGCTTCAGAAAGGA 431  
QY 2905 TCTTTTGTCTCAACCACTCAGAGATCCCACTTCGCTTAAGTTCCAGAGAGCTTTGACG 2964  
Db 432 TCTTTTGTCTCAACCACTCAGAGATCCCACTTCGCTTAAGTTCCAGAGAGCTTTGACG 491  
QY 2965 ATCGAGAGCATGCAAAAGCAGAAATCAGTCACTCTCTGGCTGTTGAACCAAGATCCAGCA 3024

Db 492 ATGGAGAGCATGCAAAAGCAGAAATCAGTCACTCTCTGGCTGTTGAACCAAGATCCAGCA 551  
QY 3025 AACGGCCACAGCCACAGAACTGCTCAAGAGTGAGTGTGCTGCCCCACCCAGATGGAGG 3084  
Db 552 AACGGCCACAGCCACAGAACTGCTCAAGAGTGAGTGTGCTGCCCCACCCAGATGGAGG 611  
QY 3085 AGTCAGAGCTGTGATGAAGTGTGTCACCAACAGCTGACCAACAGCTGGATGGAAAGGCTTACC 3144  
Db 612 AGTCAGAGCTGTGATGAAGTGTGTCACCAACAGCTGACCAACAGCTGGATGGAAAGGCTTACC 671  
QY 3145 GCACCATGATGGCCAGATCTTCTCCAGCGGATCTCCCTCGCATCGCATACACCATATG 3204  
Db 672 GCACCATGATGGCCAGATCTTCTCCAGCGGATCTCCCTCGCATCGCATACACCATATG 731  
QY 3205 ACAGCGACATCTACTGAAGGGCAACTTCTCAATCCGTCAGCCAGATGTCAGCAGCATGTGT 3264  
Db 732 ACAGCGACATCTACTGAAGGGCAACTTCTCAATCCGTCAGCCAGATGTCAGCAGCATGTGT 791  
QY 3265 GTGAAACCATCATCCGCATCTTTAAAGACATGAGCTGTTCAGTTGTGTACTTCCACTAC 3324  
Db 792 GTGAAACCATCATCCGCATCTTTAAAGACATGAGCTGTTCAGTTGTGTACTTCCACTAC 851  
QY 3325 TGCTTCCCGAAACAGACAAATATATGAGCACAACGAGCTGCCCTATTTCATGGACCA 3384  
Db 852 TGCTTCCCGAAACAGACAAATATATGAGCACAACGAGCTGCCCTATTTCATGGACCA 911  
QY 3385 GCGGATGCTGGTGTGCTTCCCTTTGACCTCGGATCCCTTTTGAAGATATGTGGCA 3444  
Db 912 GCGGATGCTGGTGTGCTTCCCTTTGACCTCGGATCCCTTTTGAAGATATGTGGCA 971  
QY 3445 GAAATAATATATTGAATTTTAAACAGATCTTGCAATAGAACGTGTGTTTCAGGCCCGCAAGT 3504  
Db 972 GAAATAATATATTGAATTTTAAACAGATCTTGCAATAGAACGTGTGTTTCAGGCCCGCAAGT 1031  
QY 3505 TAGATCGATTTTCATCCCAAGAACTTCTGGAGTGTGCATTTGATTTGCTTCACTTACCA 3564  
Db 1032 TAGATCGATTTTCATCCCAAGAACTTCTGGAGTGTGCATTTGATTTGCTTCACTTACCA 1091  
QY 3565 CCAACAGCTTCTGCCACCTGCTGAAATATCTACACTACTCTATGAAATCATCCCAAGT 3624  
Db 1092 CCAACAGCTTCTGCCACCTGCTGAAATATCTACACTACTCTATGAAATCATCCCAAGT 1151  
QY 3625 TTCAGCACTTCAGGAAAGAAATTCAGATTTTATTTGAACCATACCATGTTTATTGAAAG 3684  
Db 1152 TTCAGCACTTCAGGAAAGAAATTCAGATTTTATTTGAACCATACCATGTTTATTGAAAG 1211  
QY 3685 CAATACCTTACACTGTGGATCCAGAGATATACTCAGTCAAGTCTACATTTATTTCTGT 3744  
Db 1212 CAATACCTTACACTGTGGATCCAGAGATATACTCAGTCAAGTCTACATTTATTTCTGT 1271  
QY 3745 ATGATGCTGTGACAGAGAGCTGACGAGGAGAGAGTGGAAAGCTAAATTTTGTAACTGT 3804  
Db 1272 ATGATGCTGTGACAGAGAGCTGACGAGGAGAGAGTGGAAAGCTAAATTTTGTAACTGT 1331  
QY 3805 CTTTGTCTTCTTAATAGTCTGTGTGACTCTCAAGTTTATTTGAACAGAGGAGGATTTGC 3864  
Db 1332 CTTTGTCTTCTTAATAGTCTGTGTGACTCTCAAGTTTATTTGAACAGAGGAGGATTTGC 1391  
QY 3865 AAGATCTTATGCCAACAAATAAATTCATTAATAAACAAGGATGTTGTCACAGTTGG 3924  
Db 1392 AAGATCTTATGCCAACAAATAAATTCATTAATAAACAAGGATGTTGTCACAGTTGG 1451  
QY 3925 TGAAGTATGGCTTAAAGACCTAGAGGAGTGTGTGAGCTGTGTGAAGAAACCTGGCATCA 3984  
Db 1452 TGAAGTATGGCTTAAAGACCTAGAGGAGTGTGTGAGCTGTGTGAAGAAACCTGGCATCA 1511  
QY 3985 AGTTACAGGCTCTTATCAATTTTGGGCTTGGTTTACAAGGTGACAGCAGCAATGGAATCA 4044  
Db 1512 AGTTACAGGCTCTTATCAATTTTGGGCTTGGTTTACAAGGTGACAGCAGCAATGGAATCA 1571  
QY 4045 TCTTCCAGTTTGTGGCTTTTCATCAACAGAGGCAAGGGCTGTACCTGAAATCTCTCGAG 4104



1572 TCTTCCAGTTTGTGGCTTTTCATCAACGAAGGCAAGGGCTGTACCTGAAATCTCTCGCAG 1631  
4105 CTGAGGACAGATATGACCTGCTGATTTCCCGAGTTTACAGGGCCACAGCTCTGGGGCCAG 4164  
1632 CTGAGGACAGATATGACCTGCTGATTTCCCGAGTTTACAGGGCCACAGCTCTGGGGCCAG 1691  
4165 TTCCCACTGCTGATTTGGGGTTCAGCATAGCTATAGCAAGATATCTGCTGCTGCTCAACA 4224  
1692 TTCCCACTGCTGATTTGGGGTTCAGCATAGCTATAGCAAGATATCTGCTGCTGCTCAACA 1751  
4225 TGGAGGAATCTGTTCAATTAAGCTCTGTGACCTCTGTTGTAAGTGTGTTGTCAGATGT 4284  
1752 TGGAGGAATCTGTTCAATTAAGCTCTGTGACCTCTGTTGTAAGTGTGTTGTCAGATGT 1811  
4285 CTATGTCCAGGGCCATCAACTAACCCAGAAAATCTTGGACAGCAGGCTATCAGCAGAGAA 4344  
1812 CTATGTCCAGGGCCATCAACTAACCCAGAAAATCTTGGACAGCAGGCTATCAGCAGAGAA 1871  
4345 TCATGTAGCATGTGTCAGTCCAGAGAGAAATTAACAAGTACTCTCAGACATCATGAAA 4404  
1872 TCATGTAGCATGTGTCAGTCCAGAGAGAAATTAACAAGTACTCTCAGACATCATGAAA 1931  
4405 TCACCTATGTGGCCCTTGTCTCGGATAAAGAAAGCCATGTCAAGGTTAAAGTCTTTCCG 4464  
1932 TCACCTATGTGGCCCTTGTCTCGGATAAAGAAAGCCATGTCAAGGTTAAAGTCTTTCCG 1991  
4465 AGAAGGAAAGGACAGACAGAGAGCGTGTCTGAGACTGAACCTTTGGACCAATGACTGC 4524  
1992 AGAAGGAAAGGACAGACAGAGAGCGTGTCTGAGACTGAACCTTTGGACCAATGACTGC 2051  
4525 AGAACTGAGGACTAAAGTCACTGATGAAGGAATGCGAGAGAGCTTCCGATAATCTTG 4584  
2052 AGAACTGAGGACTAAAGTCACTGATGAAGGAATGCGAGAGAGCTTCCGATAATCTTG 2111  
4585 CAGTGCAAAATCTGAAGGGTCAATTTCTAATGCTTCAGGTTGTTGAAATCCATGGAG 4644  
2112 CAGTGCAAAATCTGAAGGGTCAATTTCTAATGCTTCAGGTTGTTGAAATCCATGGAG 2171  
4645 CAACAGTGGTTCCTCATGTCAGTGTGCTAGCCCGGAGAGCTGCAGCAGCAGCTAGGA 4704  
2172 CAACAGTGGTTCCTCATGTCAGTGTGCTAGCCCGGAGAGCTGCAGCAGCAGCTAGGA 2231  
4705 GGCCTATGAACCTCAGGTACAACTCGACTTCAGACCTCCCTTGCACACTTACATCAGA 4764  
2232 GGCCTATGAACCTCAGGTACAACTCGACTTCAGACCTCCCTTGCACACTTACATCAGA 2291  
4765 AAGCAGTGAATTTGAATTTCTGGCTGTGATCTACCCAAAGAAACAATATTACAGTTT 4824  
2292 AAGCAGTGAATTTGAATTTCTGGCTGTGATCTACCCAAAGAAACAATATTACAGTTT 2351  
4825 TATCATTAGAGTGGGATGCTGATGAACAGGCAATTTAACACAACTGTGAAGAGCTGCTGT 4884  
2352 TATCATTAGAGTGGGATGCTGATGAACAGGCAATTTAACACAACTGTGAAGAGCTGCTGT 2411  
4885 CACGCTGCCAAAGCAAGATACCTGAATAGTCTGTGATGAAATTTATACATCAAG 4944  
2412 CACGCTGCCAAAGCAAGATACCTGAATAGTCTGTGATGAAATTTATACATCAAG 2471  
4945 TAGAAAAAAGGCTGCTGTGCTATTTCTGTACAGCTATAGAGATGACTACTACAGAACT 5004  
2472 TAGAAAAAAGGCTGCTGTGCTATTTCTGTACAGCTATAGAGATGACTACTACAGAACT 2531  
5005 TATTTTAAACCTTAAAGACTGTGCTTAACCTCATTTCAAACAGACAGAGCTTATCTGGA 5064  
2532 TATTTTAAACCTTAAAGACTGTGCTTAACCTCATTTCAAACAGACAGAGCTTATCTGGA 2591  
5065 ATAATGGAATCTGTACATTCATCAATTAATTTAAATTTAAATTTAAATTTAAATTTAA 5124  
2592 ATAATGGAATCTGTACATTCATCAATTAATTTAAATTTAAATTTAAATTTAAATTTAA 2651  
5125 CAGTGGCTCACACCTTTAAATCCAGCACTTTGGGAAAGCCAGGACAGAGATGCTTGAA 5184  
2652 CAGTGGCTCACACCTTTAAATCCAGCACTTTGGGAAAGCCAGGACAGAGATGCTTGAA 2711

5185 ACCAGAGTTTGGAGCCAGCTGAGCAACAAAGCAAGACCCCATCTCTATATAAACTAAA 5244  
2712 ACCAGAGTTTGGAGCCAGCTGAGCAACAAAGCAAGACCCCATCTCTATATAAACTAAA 2771  
5245 AAAATTAGTTGGGCATGTGGCAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5304  
2772 AAAATTAGTTGGGCATGTGGCAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2831  
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2832 GATCATCTCAGCTCAGGAGTTGAGGCTGCACTGAGCTGTGACTGTGCTGCGCCACTGCACTCC 2891  
5365 AGTCTGGGCAACAGAGCAAGACCTGTCTTAAAAAAGAAAAA 5416  
2892 AGTCTGGGCAACAGAGCAAGACCTGTCTTAAAAAAGAAAAA 2943

RESULT 10

US-09-925-301-184  
; Sequence 184, Application US/09925301  
; Patent No. US20020052308A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA106  
; CURRENT APPLICATION NUMBER: US/09/925,301  
; PRIOR FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/05882  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1694  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 184  
; LENGTH: 2200  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (2096)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2140)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2157)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2181)  
; OTHER INFORMATION: n equals a,t,g, or c  
; NAME/KEY: misc feature  
; LOCATION: (2184)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-301-184

Query Match 38.8%; Score 2144.6; DB 9; Length 2200;  
Best Local Similarity 99.0%; Pred. No. 0;  
Matches 2173; Conservative 2; Mismatches 16; Indels 3; Gaps 2;

QY 3206 CAGCGACACTCAGGGCAACTTCTCAATCCGTACAGCCAGATGCGAGCATGTGTG 3265  
DB 9 CAGCGACACTCAGGGCAACTTCTCAATCCGTACAGCCAGATGCGAGCATGTGTG 68  
QY 3266 TGAACCATCATCCGCATCTTTAAAGACATGGAGCTGTTTCAAGTTGTCTTCCACTACT 3325  
DB 69 TGAACCATCATCCGCATCTTTAAAGACATGGAGCTGTTTCAAGTTGTCTTCCACTACT 128  
QY 3326 GCTTCCCGCAACAGCAATATATGACCAACCAAGCTCCCTATTTCATGGCCACAG 3385  
DB 129 GCTTCCCGCAACAGCAATATATGACCAACCAAGCTCCCTATTTCATGGCCACAG 188  
QY 3386 CGGATGCTGGTGTGATGCTTCCCTTTTGAACCTGGGATCCCTTTTGAAGATATGTGGCAAG 3445

RESULT 11  
US-10-006-285-498  
; Sequence 498, Application US/10006285  
; Publication No. US20030165854A1  
; GENERAL INFORMATION:  
; APPLICANT: Mary Jane Cunningham  
; APPLICANT: Matthew R. Kaser  
; TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS  
; FILE REFERENCE: PA-0039 US  
; CURRENT APPLICATION NUMBER: US/10/006,285



CURRENT FILING DATE: 2001-12-05  
NUMBER OF SEQ ID NOS: 514  
SOFTWARE: PERL Program  
SEQ ID NO 498  
LENGTH: 1845  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
OTHER INFORMATION: Incyte ID NC  
NAME/KEY: unbrs  
LOCATION: 467, 528, 540  
OTHER INFORMATION: a, t, c, g,  
10-006-285-498

Query Match	31.1%;	Score 1716.4;	DB 14;	Length 1845;
Best Local Similarity	94.0%;	Prod. No. 0;		
Matches 1841;	Conservative	0;	Mismatches 4;	Indels 114; Gaps 1;
3157	CCAGATCTTCTCGCAGCGCATCTCCCTGCCATCGATTACACTATGACAGGACATAC	3216		
db	1	CCAGATCTTCTCGCAGCGCATCTCCCTGCCATCGATTACACTATGACAGGACATAC	60	
3217	TGAAGGGCAACTTCTCAATCCGTACAGCCAAAGATCGCAGCAGTGTGTGAAACATCA	3276		
db	61	TGAAGGGCAACTTCTCAATCCGTACAGCCAAAGATCGCAGCAGTGTGTGAAACATCA	120	
3277	TCGCGATCTTTTAAAGACATGAGAGCTGTTTCAGTTGTGTACTCCACTACTGCTTCCCGGAA	3336		
db	121	TCCGCACTTTTAAAGACATGAGAGCTGTTTCAGTTGTGTACTCCACTACTGCTTCCCGGAA	180	
3337	ACAGACAAATATATGAGCACAACGAAGCTGCCCTATTATATGAGCACAAGCGGATGCTGG	3396		
db	181	ACAGACAAATATATGAGCACAACGAAGCTGCCCTATTATATGAGCACAAGCGGATGCTGG	240	
3397	TGATGCTTTCCTTTTGACCTCGGATCCCTTTTGCAGAGATATGTGCGAAGAAATAATATAT	3456		
db	241	TGATGCTTTCCTTTTGACCTCGGATCCCTTTTGCAGAGATATGTGCGAAGAAATAATATAT	300	
3457	TGAATTTAAACAGATATCGATAGACAGTGTGTTTACGCCCGGCAAGTTAGATCGATTTC	3516		
db	301	TGAATTTAAACAGATATCGATAGACAGTGTGTTTACGCCCGGCAAGTTAGATCGATTTC	360	
3517	ATCCCAAAGAACTTCTGGAGTGTGCATTGTGATATTGTCACTTTCACCAACCAAGCTTTC	3576		
db	361	ATCCCAAAGAACTTCTGGAGTGTGCATTGTGATATTGTCACTTTCACCAACCAAGCTTTC	420	
3577	TGCCCATGCTGAAATATATCTACATATCTATGAATATCATCAAGAGTTTCCAGACATTC	3636		
db	421	TGCCCATGCTGAAATATATCTACATATCTATGAATATCATCAAGAGTTTCCAGACATTC	480	
3637	AGGAAGAAATTCAGATATTTATTTGAAACCATACCATGTTATTGAAAGCAATCTCTTAC	3696		
db	481	AGGAAGAAATTCAGATATTTATTTGAAACCATACCATGTTATTGAAAGCAATCTCTTAN	540	
3697	ACTGTGGATCCGAGAAGATAAATCAGTCAAGTCTACATTTATCTGTATGAGTGTGTA	3756		
db	541	ACTGTGGATCCGAGAAGATAAATCAGTCAAGTCTACATTTATCTGTATGAGTGTGTA	600	
3757	CAGAGACTCGCAGGAGAGAGTGGAGCTAAATTTTGTAAATCTGTCTTTGTCTTCTA	3816		
db	601	CAGAGAGCTCGCAGGAGAGAGTGGAGCTAAATTTTGTAAATCTGTCTTTGTCTTCTA	660	
3817	ATAGTCTGTGCGACTCTACAGTTTATTGAAACAGAGGAGATTTGCAAGATCTTATGC	3876		
db	661	ATAGTCTGTGCGACTCTACAGTTTATTGAAACAGAGGAGATTTGCAAGATCTTATGC	720	
3877	CAACATAAATTCATTATAAACAGAAACAGATATTCACAGTTTGGTGAAGTATGGCT	3936		
db	721	CAACATAAATTCATTATAAACAGAAACAGATATTCACAGTTTGGTGAAGTATGGCT	780	
3937	TAAAGACCTAGAGGAGGTCTTGCATGTTTGAAGAACTTCGCGATCAAGTTTACAGTCT	3996		



Best Local Similarity 87.0%; Pred. No. 1.8e-90;  
Matches 410; Conservative 0; Mismatches 61; Indels 0; Gaps 0

CURRENT FILING DATE: 2001-11-16  
NUMBER OF SEQ ID NOS: 2606  
SOFTWARE: Corixa Invention Disclosure Database  
SEQ ID NO 753  
LENGTH: 519  
TYPE: DNA  
ORGANISM: Homo sapiens  
JS-09-998-598-753

Query Match 9.4%; Score 517.4; DB 9; Length 519;  
Best Local Similarity 99.8%; Pred. No. 1.4e-129;  
Matches 518; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 3464 AAAACGATCTCATAGAACGTGGTTCAGCCCGCGCAGTAGATCGATTTCATCCAA 3523  
B 1 AAACGATCTCATAGAACGTGGTTCAGCCCGCGCAGTAGATCGATTTCATCCAA 60  
Y 3524 AGAAGTTCTGGAGTGCAATTTGATTTGTCACCTTCTACCACCAACAGCTTTCTGCCCAC 3583  
B 61 AGAAGTTCTGGAGTGCAATTTGATTTGTCACCTTCTACCACCAACAGCTTTCTGCCCAC 120  
Y 3584 TGCTGAATTAATCTACATATCTATGAATCATCCAGAGTTTCAGGACTTCAGGAAG 3643  
B 121 TGCTGAATTAATCTACATATCTATGAATCATCCAGAGTTTCAGGACTTCAGGAAG 180  
Y 3644 AAATACAGTATTTATTTGAACCAATACATGTTATTTGAACAATATCTTTACACTGCG 3703  
B 181 AAATACAGTATTTATTTGAACCAATACATGTTATTTGAACAATATCTTTACACTGCG 240  
Y 3704 GATCCAGAAGATAAAGTCAAGTCAATTTATGATTTATGATGCTGTGCAGAGAA 3763  
B 241 GATCCAGAAGATAAAGTCAAGTCAATTTATGATTTATGATGCTGTGCAGAGAA 300  
Y 3764 GCTGACGAGGAGAGTGGAGCTAAATTTGTAATCTGCTTTGCTTCTTAATAGTCT 3823  
B 301 GCTGACGAGGAGAGTGGAGCTAAATTTGTAATCTGCTTTGCTTCTTAATAGTCT 360  
Y 3824 GTGTCGACTCTCAAGTTTTATTTGAACAGAGGAGATTGCAAGATCTTAATGCCAACAT 3883  
B 361 GTGTCGACTCTCAAGTTTTATTTGAACAGAGGAGATTGCAAGATCTTAATGCCAACAT 420  
Y 3884 AATTCATTAAATAACAGAAAACAGTATTGACAGTGTGGAAGTATGCTTAAAGA 3943  
B 421 AATTCATTAAATAACAGAAAACAGTATTGACAGTGTGGAAGTATGCTTAAAGA 480  
Y 3944 CCTAGAGGAGTGTGGAGTCTGTGAAGAAACTCGGCAT 3982  
B 481 CCTAGAGGAGTGTGGAGTCTGTGAAGAAACTCGGCAT 519

RESULT 14  
US-10-006-285-340  
Sequence 340, Application US/10006285  
Publication No. US20030165854A1  
GENERAL INFORMATION:  
APPLICANT: Mary Jane Cunningham  
TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS  
FILE REFERENCE: PA-0039 US  
CURRENT APPLICATION NUMBER: US/10/006,285  
PRIORITY FILING DATE: 2001-12-05  
NUMBER OF SEQ ID NOS: 514  
SOFTWARE: PERL Program  
SEQ ID NO 340  
LENGTH: 471  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20030165854A1 237271\_Rn.1  
US-10-006-285-340

Query Match 6.8%; Score 373.4; DB 14; Length 471;  
Best Local Similarity 54.9%; Pred. No. 5.6e-89;  
Matches 380; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

Y 4820 GTTTTATCATTTAGAGTGGATGCTGATGAACAGGCAATTTAACACAACTGTGAAGCAGCT 4879  
B 1 GTTTTATCATTTAGAGTGGATGCTGATGAACAGGCAATTTAACACAACTGTGAAGCAGCT 60  
Y 4880 GCTGTACCGCTGCCAACCAAGATACCTCAATAGTCTGTGTGAATTTATAACAT 4933

Best Local Similarity 87.0%; Pred. No. 1.8e-90;  
Matches 410; Conservative 0; Mismatches 61; Indels 0; Gaps 0

CURRENT FILING DATE: 2001-11-16  
NUMBER OF SEQ ID NOS: 2606  
SOFTWARE: Corixa Invention Disclosure Database  
SEQ ID NO 753  
LENGTH: 519  
TYPE: DNA  
ORGANISM: Homo sapiens  
JS-09-998-598-753

Query Match 9.4%; Score 517.4; DB 9; Length 519;  
Best Local Similarity 99.8%; Pred. No. 1.4e-129;  
Matches 518; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Y 3464 AAAACGATCTCATAGAACGTGGTTCAGCCCGCGCAGTAGATCGATTTCATCCAA 3523  
B 1 AAACGATCTCATAGAACGTGGTTCAGCCCGCGCAGTAGATCGATTTCATCCAA 60  
Y 3524 AGAAGTTCTGGAGTGCAATTTGATTTGTCACCTTCTACCACCAACAGCTTTCTGCCCAC 3583  
B 61 AGAAGTTCTGGAGTGCAATTTGATTTGTCACCTTCTACCACCAACAGCTTTCTGCCCAC 120  
Y 3584 TGCTGAATTAATCTACATATCTATGAATCATCCAGAGTTTCAGGACTTCAGGAAG 3643  
B 121 TGCTGAATTAATCTACATATCTATGAATCATCCAGAGTTTCAGGACTTCAGGAAG 180  
Y 3644 AAATACAGTATTTATTTGAACCAATACATGTTATTTGAACAATATCTTTACACTGCG 3703  
B 181 AAATACAGTATTTATTTGAACCAATACATGTTATTTGAACAATATCTTTACACTGCG 240  
Y 3704 GATCCAGAAGATAAAGTCAAGTCAATTTATGATTTATGATGCTGTGCAGAGAA 3763  
B 241 GATCCAGAAGATAAAGTCAAGTCAATTTATGATTTATGATGCTGTGCAGAGAA 300  
Y 3764 GCTGACGAGGAGAGTGGAGCTAAATTTGTAATCTGCTTTGCTTCTTAATAGTCT 3823  
B 301 GCTGACGAGGAGAGTGGAGCTAAATTTGTAATCTGCTTTGCTTCTTAATAGTCT 360  
Y 3824 GTGTCGACTCTCAAGTTTTATTTGAACAGAGGAGATTGCAAGATCTTAATGCCAACAT 3883  
B 361 GTGTCGACTCTCAAGTTTTATTTGAACAGAGGAGATTGCAAGATCTTAATGCCAACAT 420  
Y 3884 AATTCATTAAATAACAGAAAACAGTATTGACAGTGTGGAAGTATGCTTAAAGA 3943  
B 421 AATTCATTAAATAACAGAAAACAGTATTGACAGTGTGGAAGTATGCTTAAAGA 480  
Y 3944 CCTAGAGGAGTGTGGAGTCTGTGAAGAAACTCGGCAT 3982  
B 481 CCTAGAGGAGTGTGGAGTCTGTGAAGAAACTCGGCAT 519

RESULT 15  
US-10-062-674-1525  
Sequence 1525, Application US/10062674  
Publication No. US20040005559A1  
GENERAL INFORMATION:  
APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.  
TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS  
FILE REFERENCE: PA-0026-1 CIP  
CURRENT APPLICATION NUMBER: US/10/062,674  
CURRENT FILING DATE: 2002-01-30  
PRIOR APPLICATION NUMBER: US 09/625,102  
PRIOR FILING DATE: 2000-07-24  
NUMBER OF SEQ ID NOS: 2217  
SOFTWARE: PERL Program  
SEQ ID NO 1525  
LENGTH: 691  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20040005559A1 1176865.1  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1) ... (691)  
OTHER INFORMATION: a, t, c, g, or other  
US-10-062-674-1525

Query Match 6.7%; Score 368.4; DB 15; Length 691;  
Best Local Similarity 54.9%; Pred. No. 5.6e-89;  
Matches 380; Conservative 0; Mismatches 31; Indels 1; Gaps 1;

Y 4820 GTTTTATCATTTAGAGTGGATGCTGATGAACAGGCAATTTAACACAACTGTGAAGCAGCT 4879  
B 1 GTTTTATCATTTAGAGTGGATGCTGATGAACAGGCAATTTAACACAACTGTGAAGCAGCT 60  
Y 4880 GCTGTACCGCTGCCAACCAAGATACCTCAATAGTCTGTGTGAATTTATAACAT 4933

Db 61 GCTGTCACGCTGCCAAAGCAAGATACCTCAAATTAGTCTGTGATGAAATTTATAACAT 120  
2Y 4940 CAAAGTAGAAAAAAGGTGCTGTGCTATTCTGTACAGCTATAGAGATGACTACTACAG 4999  
Db 121 CAAAGTAGAAAAAAGGTGCTGTGCTATTCTGTACAGCTATAGAGATGACTACTACAG 180  
2Y 5000 AATCTTATTTTAAACCCCTAAAGAACTGTCGTTAAACCTCATTTCAAACACAGAGAGCTTATA 5059  
Db 181 AATCTTATTTTAAACCCCTAAAGAACTGTCGTTAAACCTCATTTCAAACACAGAGAGCTTATA 240  
2Y 5060 CTGGAATTAATGGAATGTTGTACATTCATCAATAATTTAAATTTAAATTTAAAGAGAGCT 5119  
Db 241 CTGGAATTAATGGAATGTTGTACATTCATCAATAATTTAAATTTAAATTTAAAGAGAG -NNN 299  
2Y 5120 GGGTGCAGTGGCTCACACCTTTAATCCAGCACTTTGGGAAGCCAAAGGCAGGAAGACTGC 5179  
Db 300 NNN 359  
2Y 5180 TTGAAAACAGAGATTGTGAGACCGCTGAGCAACAAAGCAAGACCCCATCTCTATAAAA 5239  
Db 360 NNN 419  
2Y 5240 CTAAAAAAATTAGTTGGGCATGGTGGCACATGCTGTAGTCCAGCTACTCCAGAGGCTG 5299  
Db 420 NNN 479  
2Y 5300 AGATGGATCATCTGAGCCTCAGGAGGTTGAGGCTGAGCTGTGACTGCGCCACTGC 5359  
Db 480 NNN 539  
QY 5360 ACTCCAGTCTGGACACACAGAGCAAGACCCCTGCTTAAAAAAGAAAAAATTT 5419  
Db 540 NNN 599  
QY 5420 TTTTCTAAGAGCTGCTCTCAAAAGTTGAGCTTTGTTAGTTTTCATGTGTAATATT 5479  
Db 600 NNNNNNAAGAGCTGCTCTCAAAAGTTGAGCTTTGTTAGTTTTCATGTGTAATATT 659  
QY 5480 ATAAATTTATCTTTGGGATATATAATGCT 5511  
Db 660 ATAAATTTATCTTTGGGGTATAATAATGCT 691

Search completed: March 22, 2004, 01:47:11  
Job time : 1247 secs

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3M protein - nucleic search, using frame\_plus\_p2n model

run on: March 21, 2004, 22:14:49 ; Search time 175 Seconds  
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5229.223 Million cell updates/sec

Title: US-09-515-806A-2  
Perfect score: 8544  
Sequence: 1 MAGCGAGPGRDPPESVP.....KKVSVFLYSYRDDYRILF 1649

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Fgapop 6.0 , Fgapext 7.0  
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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	480.5	5.6	2729	1 US-07-938-782A-1	Sequence 1, Appli
2	480.5	5.6	2729	1 US-08-630-524-1	Sequence 1, Appli
3	480.5	5.6	2729	5 PCT-US93-08131-1	Sequence 1, Appli
4	470	5.5	1887	4 US-09-799-875-18	Sequence 16, Appl
5	470	5.5	2870	4 US-09-799-875-16	Sequence 1, Appli
6	470	5.5	2891	4 US-09-578-441-1	Sequence 785, App
7	443	5.2	244	4 US-09-016-434-785	Sequence 1, Appli
8	416	4.9	2628	1 US-08-143-219-1	Sequence 8, Appli
9	413.5	4.8	2562	2 US-08-436-771-8	Sequence 8, Appli
10	413.5	4.8	2562	2 US-08-434-998-8	Sequence 8, Appli
11	413.5	4.8	2562	2 US-08-487-797-8	Sequence 8, Appli
12	413.5	4.8	2562	5 PCT-US95-02058-8	Sequence 8, Appli

13	358	4.2	2827	4 US-09-554-726A-11	Sequence 11, Appl
14	358	4.2	2827	4 US-09-554-726A-20	Sequence 20, Appl
15	321	3.8	4307	4 US-09-803-671B-1	Sequence 1, Appli
16	317.5	3.7	2157	4 US-09-371-338-16	Sequence 16, Appl
17	317	3.7	2527	4 US-09-371-338-20	Sequence 20, Appl
18	305.5	3.6	2076	4 US-09-554-726A-1	Sequence 1, Appli
19	305	3.6	2155	4 US-09-371-338-8	Sequence 8, Appli
20	303.5	3.6	4403765	3 US-09-103-840A-2	Sequence 2, Appli
21	303.5	3.6	4411529	3 US-09-103-840A-1	Sequence 10, Appl
22	302.5	3.5	802	4 US-09-371-338-10	Sequence 10, Appl
23	300	3.5	2193	4 US-09-371-338-12	Sequence 12, Appl
24	296.5	3.5	804	4 US-09-371-338-14	Sequence 14, Appl
25	295.5	3.5	804	4 US-09-371-338-22	Sequence 22, Appl
26	294.5	3.4	804	4 US-09-371-338-18	Sequence 18, Appl
27	292	3.4	1744	4 US-09-685-462-9	Sequence 9, Appli
28	284.5	3.3	3089	1 US-08-472-934-5	Sequence 5, Appli
29	284.5	3.3	3089	2 US-08-323-460A-5	Sequence 5, Appli
30	284.5	3.3	3089	3 US-08-461-146C-5	Sequence 5, Appli
31	284.5	3.3	3089	3 US-08-461-145C-5	Sequence 5, Appli
32	284.5	3.3	3089	4 US-08-628-829-9	Sequence 9, Appli
33	284.5	3.3	3332	4 US-09-423-890-11	Sequence 11, Appl
34	283	3.3	1542	4 US-09-345-473E-13	Sequence 13, Appl
35	282	3.3	3201	2 US-09-211-930-1	Sequence 1, Appli
36	282	3.3	3201	3 US-09-340-993-1	Sequence 1, Appli
37	282	3.3	3201	4 US-09-468-442-1	Sequence 1, Appli
38	282	3.3	3268	4 US-09-688-189B-1	Sequence 1, Appli
39	282	3.3	3268	4 US-09-291-417D-1	Sequence 1, Appli
40	278.5	3.3	1935	4 US-09-423-890-5	Sequence 5, Appli
41	277.5	3.2	2119	4 US-09-167-206-1	Sequence 1, Appli
42	277	3.2	5236	3 US-09-359-757-1	Sequence 1, Appli
43	273	3.2	7685	4 US-09-221-017B-1092	Sequence 1092, Ap
44	272	3.2	1500	4 US-09-685-462-1	Sequence 1, Appli
45	270	3.2	2028	2 US-09-211-930-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1  
US-07-938-782A-1  
; Sequence 1, Application US/07938782A  
; Patent No. 5525513  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Jane J.  
; APPLICANT: London, Irving M.  
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated  
; TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha kinase  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: US  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/938,782A  
; FILING DATE: 31-AUG-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: WU101CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404)873-8794  
; TELEFAX: (404)873-8795  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:

LENGTH: 2729 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 ORGANISM: Rabbit  
 CELL TYPE: Reticulocytes

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 113..2149  
 OTHER INFORMATION: /note= "Expression of HRI  
 mRNA in Human erythroid cells, using as the  
 OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides 113  
 OTHER INFORMATION: to 2149."  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 229..249  
 OTHER INFORMATION: /note= "Primer used in the  
 amplification of human HRI cDNA sequence  
 OTHER INFORMATION: using the rabbit HRI cDNA sequence."

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 543..560  
 OTHER INFORMATION: /note= "Primer used in the  
 amplification of human HRI cDNA sequence  
 OTHER INFORMATION: using the rabbit HRI cDNA sequence."

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 448..468  
 OTHER INFORMATION: /note= "Primer used in the  
 amplification of human HRI cDNA sequence  
 OTHER INFORMATION: using the rabbit HRI cDNA sequence."

FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: 1009..1031  
 OTHER INFORMATION: /note= "Primer used in the  
 amplification of a human HRI cDNA sequence  
 OTHER INFORMATION: using the rabbit HRI cDNA sequence."

PUBLICATION INFORMATION:  
 AUTHORS: Chen, Jane J.  
 TITLES: Cloning of the cDNA of the heme-  
 regulated eukaryotic initiation factor  
 TITLE: 2alpha (eIF-2alpha) kinase of rabbit reticulocytes:  
 TITLE: Homology to yeast GCN5 protein kinase and human  
 TITLE: double-stranded-RNA-dependent  
 JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
 VOLUME: 88  
 PAGES: 7729-7733  
 DATE: September-1991

US-09-515-806A-1  
 US-09-515-806A-2

Alignment Scores:  
 Pred. No.: 1.33e-38 Length: 2729  
 Score: 480.50 Matches: 184  
 Percent Similarity: 43.91% Conservative: 97  
 Best Local Similarity: 28.75% Mismatches: 241  
 Query Match: 5.62% Indels: 119  
 DB: 1 Gaps: 29

US-09-515-806A-2 (1-1649) x US-07-938-782A-1 (1-2729)

QY 580 GlnArgGlnPheSerArgTyrPheIleGluPheGluGluLeuGlnLeuLeuGlyLysGly 599  
 Db 590 GAAGCAGACACCTCAGCATCTTGAATGATGTTGAAGAGCTCTCCATCCTGGGAAAAGGT 649  
 QY 600 AlaPheGlyAlaValIleLysValGlnLysLeuAspGlyCysCysTyrAlaValLys 619  
 Db 650 GGCTATGGCGAGTGTACAAAGTTCAGGATAAAATAGATGCCAGTATTATGCAATTAAA 709

QY 620 ArgIleProIleAsnProAlaSerArg---GlnPheArgArgIleLysGlyGluValThr 638  
 Db 710 AAAATTCTGATTAAAGGTGCAATATAAACAAGTTCATGAAGTATTACGAGAAGTGA 769  
 QY 639 LeuLeuSerArgLeuHisGluAsnIleValArgTyrTyrAsnAlaTirPileGluArg 658  
 Db 770 GTGCTGGCGGCTCCAGCACCTAATATCGTAGCTATCACACCGCGTGTATAGCAT 829  
 QY 659 ---HisGluArgProAlaGlyProGlyThrPro-----ProProAspSerGlyProLeu 675  
 Db 830 GTCCACGTTTCAGTTCAAGCAGACAGAGTTCGATTCAGTTGCTTCTCGAAGTGTCT 889  
 QY 676 Ala-----LysAspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeu 693  
 Db 890 TCTGACACGAGAGACAGACAGATCAATATGGTTAAATATGTTAAATATGTAAGCAGCAGCTCA 949  
 QY 694 AspSerValGluAlaAlaProProProIleLeuSerSerValGluTyrSerThr 713  
 Db 950 TCCATTATTTCGCTGAGTCTCCACAGAAAAGAAAATCTCTGACGAATGTGCCGTT 1009  
 QY 714 SerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGly 727  
 Db 1010 GAGAGTCAGAAATAACAACTGGTGAACCTACACCACTTAGTGTGAGGACACACCGT 1069  
 QY 728 ProGlySerSerAspAspGluAspAspGluHisGlyGlyValPheSerGln 747  
 Db 1070 GAGTTGAAATCGTCCACGAG-----CGCAAGAGAGACCGCTCGATCGTGAGCGT 1120  
 QY 748 SerPheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsn 767  
 Db 1121 CAGCTACTGTTGGGCATAACTCAGACGTAGAA-----GAGATTTCACG 1165  
 QY 768 SerLysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGlu 787  
 Db 1166 TCCCGGAGGAATCTTCTGAGGAGACTTAAGCGGTTCGCG----- 1207  
 QY 788 ProSerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCys 805  
 Db 1208 -----CACACAGAGTGCAGTACCACCTGCTGCATATCCATGATCCAGATCGGTGTC 1258  
 QY 806 GluLysSer-----ThrLeuArgAspThrIleAsp 815  
 Db 1259 GAGCTGTCCTGTGGGACTGGATCGCGGAGAGAACAGCGCGGAGAGTGCCTGGAC 1318  
 QY 816 GlnGlyLeu-----TyrArgAspThrValArgLeuTyrPheArgLeuGluLeu 833  
 Db 1319 GAATCTGCTGCTCTTATGTTATGTTGTCAGTGTTCACAAATAATTTTCAAGAACTGGTG 1378  
 QY 834 AspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsn 853  
 Db 1379 GAAGTGTGTTTACATACATACATGCGCATCGTGCACAGAGACCTGAAGCTAGAAAT 1438  
 QY 854 IlePheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAlaThrAsp 872  
 Db 1439 ATTTTCTTCATGCTCCTGATCAACAAGTGAAATAGGAGACTTTGGTCTGGCC----- 1492  
 QY 873 HisLeuAlaPheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892  
 Db 1493 -----TCGCGCGACATCATCCAGAAATCGCGCCCGGACAGCAGAAACGGG 1540  
 QY 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911  
 Db 1541 GAGAGAGCACCCACACACACTTCCCGAGTGGGCACCTGTCTGTACGCTCGCCCGCAGCAG 1600  
 QY 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931  
 Db 1601 TTGGAGAGA-----TCGAGTATGATGCCAGTACAGATGATACAGCTCGCGCGTG 1651  
 QY 932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951  
 Db 1652 ATCTCTCTGGAGCTC---TTCCAGCCCTTCGGGACAGAGATGAGCGGCGAGAGGTCCTG 1708

952 AsnGlnLeuArg-----AspProThrSerProLysPheProGluAspPhe 966  
1709 ACGGGCTGGAGCTGGCGCATACCGACTCCCTCAGTAAGAGTGGCG----- 1759  
967 AspAspGlyGluHisAlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspPro 986  
1760 -----GGCGAGGCGCAAGTACGTCACGCTGCTGACAGGAGGAAACCG 1801  
987 AlalysArgProThrAlaThrGluLeuLeuLysSerGluLeuLeuProProPro----- 1004  
1802 TCCAGAGCGCGCTGGCGCTTACGCTGCTGACAGTGAAGTCTTCCAGAACTCCGCGCAT 1861  
1005 -----GlnMet-----GluLysSerGluLeuHisGluValLeu 1015  
1862 GTTAACCTCACCTACAGATGAAGATAATAGACAGAGAAAGAAATCAGAGACTCAAG 1921  
1016 HisHisThrLeuThrAsnValAspGlyLysAlaThrArgThrMetMetAlaGlnIlePhe 1035  
1922 AAGCAGTGGAGCTCTCTCCAGCGCGGAGGGTGGAGGTGA-CAGGCG----- 1971  
1036 SerGlnArgIleSerProAlaIleAspTyThrTyAspSerAspIleLeuLysGlyAsn 1055  
1972 ---AGCGGAGAGCTCGCTGAGCGCTCAGTCCGCGCAGTCAC-----AGGGGAAG 2022  
1056 PheSerIleArgThrAlaLysMetGlnGlnHisValCysGluThrIleIleArgIlePhe 1075  
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1076 LysArgHisGlyAlaValGlnLeuCysThrProLeuLeuLeuProArgAsnArgGlnIle 1095  
2080 AGGGCGCATAT-----CCTCACTTGGAAATCACTC 2109  
1096 TyrGluHisAsnGluAlaAlaLeuPheMet-----AspHisSerGlyMetLeu 1111  
2110 AGCGCGCATGACTCTCCCTCATCTCTCTTCCGGAGGTACTCTCTGTGACCTCTG 2169  
1112 Val-MetLeuProPheAspLeuArgIle---ProPhe----- 1122  
2170 GTGACTGTCTCCATTAACCTTACGCTTTCTCTTCTTCCGCAAGTCCCATTCCTG 2229  
1123 -AlaArgTyValAlaArgAsnAsnIleLeu-----AsnLeuLysArgTyCysIleG 1140  
2230 AGCTCTTACCTAGCAATTAATACTTAGGTATCGGTCTCATCTCTCTCTCTTGA 2289  
1140 u-----ArgValPheArg-ProArgLysLeuAspArgPheHisProLys 1154  
2290 ATCTTGGCCACTCGCTCTTATAGAGCAGACTCACTGCCCGCGCACCCACCCCAAGG 2345

RESULT 2  
US-08-630-524-1  
Sequence 1, Application US/08630524  
Patent No. 5690930  
GENERAL INFORMATION:  
APPLICANT: Chen, Jane J.  
APPLICANT: London, Irving M.  
TITLE OF INVENTION: DNA Encoding the Heme-Regulated  
TITLE OF INVENTION: Eukaryotic Initiation Factor 2 alpha kinase  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Patrea L. Pabst  
STREET: 2800 One Atlantic Center  
STREET: 1201 West Peachtree Street  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: US  
ZIP: 30309-3450  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,524

FILING DATE: 10-APR-1996  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/938,782  
FILING DATE: 31-AUG-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: WU101CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)873-8794  
TELEFAX: (404)873-8795  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2729 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
ORGANISM: Rabbit  
CELL TYPE: Reticulocytes  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 113..2149  
OTHER INFORMATION: /note= "Expression of HRI  
OTHER INFORMATION: mRNA in Human erythroid cells, using as the  
OTHER INFORMATION: probe rabbit HRI cDNA from nucleotides 113  
OTHER INFORMATION: to 2149."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 229..249  
OTHER INFORMATION: /note= "Primer used in the  
OTHER INFORMATION: amplification of human HRI cDNA sequence  
OTHER INFORMATION: using the rabbit HRI cDNA sequence."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 543..560  
OTHER INFORMATION: /note= "Primer used in the  
OTHER INFORMATION: amplification of human HRI cDNA sequence  
OTHER INFORMATION: using the rabbit HRI cDNA sequence."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 448..468  
OTHER INFORMATION: /note= "Primer used in the  
OTHER INFORMATION: amplification of human HRI cDNA sequence  
OTHER INFORMATION: using the rabbit HRI cDNA sequence."  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1009..1031  
OTHER INFORMATION: /note= "Primer used in the  
OTHER INFORMATION: amplification of a human HRI cDNA sequence  
OTHER INFORMATION: using the rabbit HRI cDNA sequence."  
PUBLICATION INFORMATION:  
AUTHORS: Chen, Jane J.  
AUTHORS: London, Irving M.  
TITLE: Cloning of the cDNA of the heme-  
TITLE: regulated eukaryotic initiation factor  
TITLE: 2alpha (eif-2alpha)kinase of rabbit reticulocytes:  
TITLE: Homology to yeast GCN2 protein kinase and human  
TITLE: double-stranded-RNA-dependent  
JOURNAL: Proc. Natl. Acad. Sci. U.S.A.  
VOLUME: 88  
PAGES: 7729-7733  
DATE: September-1991  
US-08-630-524-1

Alignment Scores: 1.33e-38 Length: 2729  
Pred. No.: 480.50 Matches: 184  
Score:



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percent Similarity: 43.91%      Conservative: 97
est Local Similarity: 28.75%    Mismatches: 241
very Match: 5.62%             Indels: 119
B: 1                           Gaps: 29

S-09-515-806A-2 (1-1649) x US-08-630-524-1 (1-2729)

y 580 GlnArgGlnPheSerArgTyrPheLeuGluPheGluGluLeuGlnLeuLeuGlyGly 599
b 590 GAAGACACAGACCTTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 649
y 600 AlapheLeuValAlaValLeuValGlnAsnLysLeuAspGlyCysCysTyrAlaValLys 619
b 650 GGCTATGGCCAGCTGACAGGTGACAGATTAATTAATTAATTAATTAATTAATTAATTA 709
y 620 ArgileProleAsnProLaserArg---GlnPheArgArgGileGlyGlyValThr 638
b 710 AAAATTCGATTAAAGGTGCACTAAACAGATTCGATGAAGATTAATACGAGAAGTGAAA 769
y 639 LeuLeuSerArgLeuHisGluAsnLeuValArgTyrTyrAsnAlaTyrPileGluArg 658
b 770 GTGCTGGCGGCTTCAGACCCCTATATCTAGGCTATCACCAGCTGGATAGAGCAT 829
y 659 ---HisGluArgProAlaGlyProGlyThrPro-----ProProAspSerGlyProLeu 675
b 830 GTCCACCTTCACGTTCAAGCAGACAGATTCGGATTCAGTTGCTTCTCTCGAAGTGCTC 889
y 676 Ala-----LysAspPheArgAlaAlaArgGlyGlnProLaserAspThrAspGlyLeu 693
b 890 TCTGACCAGGAAGACAGAGATCAATATGTTGTTAAATAATGATGACAGACGAGCTCA 949
y 694 AspSerValGluAlaAlaProProLleLeuSerSerSerValGluTyrPheThr 713
b 950 TCCATTATTTTCGTGATGTTCTCCCAAGAAAAGAAAATCTCTGACGAATGTGCCGTT 1009
y 714 SerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGly 727
b 1010 GAGAGTCAGATAACAACTGGTGAACACACCACTTACTGCTGTGGGACACCCGT 1069
y 728 ProGlySerSerAspGluAspAspAspGluAspGluHisGlyGlyValPheSerGln 747
b 1070 GAGTTTGAATCGTCCAGGAG-----CGCAAGAGACGCGCTCGATCGTGAGCGGT 1120
y 748 SerPheLeuProLaserAspSerGluSerAspLeilePheAspAsnGluAspGluAsn 767
b 1121 CAGCTACTGTTCCGGCATTAACCTCAGACGTAGAA-----GAGGATTTACAG 1165
y 768 SerLysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGlu 787
b 1166 TCCGGGAGGAACTCTTGAGGAGACTTAAGCGCTTGCGG-----1207
y 788 ProSerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCys 805
b 1208 -----CACACAGAGGTGCGATACCACTGATGCTGATATCCAGATGCGAGCTGTGC 1258
y 806 GluLysSer-----ThrLeuArgAspThrIleAsp 815
b 1259 GAGCTGCTCTGTGGACTGATCGCCGAGAGGAAACAGCGCGAGCGGAGAGTGGTGAC 1318
y 816 GlnGlyLeu-----TyrArgAspThrValArgLeuTyrPheArgLeuGluLeuLeu 833
b 1319 GAATCGCTCTCTTATGTTATGTTGATGTTGCAACAAAAATTTTCAAGAACTGGTG 1378
y 834 AspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsn 853
b 1379 GAAGGTGTTTTCATACATACATGATGGGATCGTGCACAGACCTTGAGCTGAGAAAT 1438
y 854 IlePheLeuAspSer---AspAspHisValLysIleGlyAspPheGlyLeuAlaThrAsp 872
b 1439 ATTTTCTTCATGTCCTGATCAACAAGTGAATAAGAGACTTGTGCTGGCC-----1492
y 873 HisLeuAlaPheSerAlaSerLysGlnAspAspGlnThrGlyAspLeuIleLysSer 892

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## RESULT 3

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PCT-US93-08131-1
; Sequence 1, Application PC/TUS9308131
; GENERAL INFORMATION:
; APPLICANT: Massachusetts Institute Of Technology
; TITLE OF INVENTION: DNA Encoding the Heme-Regulated
; NUMBER OF INVENTION: Eukaryotic Initiation Factor 2 alpha Kinase
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street

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1541 GAGAGACACCACACACACTTCCCGAGTGGGCACTCTGTAGGCTGCCCGACAG 1500
1542 ValGlnGlySerThrLysSerAlaTyranGlnLysValAspLeuPheSerLeuGlyIle 931
1601 TTGAAGA--TCGAGATGATGATGCACAGTACAGCATGTACAGCGTGCGCGTG 1651
932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951
1652 ATCTGCTGGAGCTC---TTCAGCCCTTCGGGACAGAGATGGAGCGGCGAGGTCCTG 1708
952 AsnGlnLeuArg-----AspProThrSerProLysPheProGluAaspPhe 966
1709 ACGGCGCTGGAGCTGGCCGCATACCCGACTCCCTCAGTAAGAGTGCCTG----- 1759
967 AspAspGlyGluHisAlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspPro 986
1760 -----GGCAGGCCAAGTACGTCCTGAGTCTGACCGAGGAGGACGCG 1801
987 AlalysArgProThrAlaThrGluLeuLysSerGluLeuLeuProProPro----- 1804
1802 TCCCAGCGGCGCTGGCCCTTCAGCTGCTGCAGAGTAGACTCTTCAGAACTCCGCGCAT 1861
1005 -----GlnMet-----GluGluSerGluLeuHisGluValLeu 1015
1862 GTTAACCTCACCTACAGATGAGATAATAGAGCGAGGAAAAGAAATCGAGGAATTCAAG 1921
1016 HisHisThrLeuThrAsnValAspGlyLysAlaTyrArgThrMetMetAlaGlnIlePhe 1035
1922 AAGCAGCTGAGCTCTCTCTCCAGGCGCCGAGGGGTGAGGAGTGA-CAGGCG----- 1971
1036 SerGlnArgIleSerProAlaIleAspTyrThrTyrAspSerAspIleLeuLysGlyAsn 1055
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2023 TGGACTTGCACTTGCAAGCTCAACTGGAATGGACAATTTCAAAGCTCCTGAGG---TTC 2079
1076 LysArgHisGlyAlaValGlnLeuCysThrProLeuLeuLeuProArgAsnArgGlnIle 1095
2080 AGCGGGCATANT-----CCTCACTTGGAACTCACTC 2109
1096 TyrGluHisAsnGluAlaLaLeuPheMet-----AspHisSerGlyMetLeu 1111
2110 AGCCCGCATGACTCCCCCTCATCTGCTGCTCTCCCGAGGTACTCTCTGTTGACCTCTG 2169
1112 Val-MetLeuProPheAspLeuArgIle---ProPhe----- 1122
2170 GTGACTGCTCCCAATTAACCTTACGCTTTTCCCTTTCCATTTCGCAAGTCCCATTCCTG 2229
1123 -AlaArgTyrValAlaArgAsnIleLeu-----AsnLeuLysArgTyrCysIleGI 1140
2230 AGCTCTTACCTAAGCATTAACATAATCTTAGATATCGGTCTCCCATTTCTTCTCCTTTGA 2289
1140 u-----ArgValPheArg-ProArgLysLeuAspArgPheHisProLys 1154
2290 ATCTGGGCCACTCGCTCTTTTAGAGCACACTCACTGCCCCGCCACCACCAAGG 2345

RESULT 4
US-09-799-875-18
; Sequence 18, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059

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; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 1887
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-875-18

Alignment Scores:
Pred. No.:      8,16e-38      Length:      1887
Score:          470.00      Matches:      161
Percent Similarity: 47.03%    Conservative: 69
Best Local Similarity: 32.92% Mismatches:     185
Query Match:      5.50%      Indels:       74
DB:              4          Gaps:        22

US-09-515-806A-2 (1-1649) x US-09-799-875-18 (1-1887)

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Db 445 ATCATGATCAAGGGAGTAGCCTTGGAAAGCACAACCT-----TCACGTTACTTAAATGAA 498

Qy 590 PheGluGluLeuGlnLeuLeuGlyLVsGlyAlaPheGlyAlaValIleIysValGlnAsn 609
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Qy 610 LysLeuAspGlyCysCysTyrAlaValIysArgIleProIleAsnProIleSerArgGln 629
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Qy 630 Phe---ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisIleGluAsnIle 648
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Db 679 GTTGGCTATCACACCGCTGGATAGAA---CATGTTTCATGTGATTTCAGCA----- 726

Qy 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla--- 687
Db 727 -----CGACAGAGCTCCCATTTGAGTTGCCATCTCTG 759

Qy 688 -----SerAspThrAsp 691
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Qy 692 GlyLeuAspServAlGluAlaAlaAlaProProIleLeuSerSerVal---Glu 710
Db 820 AGCAGCTCATTCATATCTTTGTCGAGCCACCCAGAAAGAAAGAAACCCGCTTTGGAGAA 879

Qy 711 TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
Db 880 TCTGACACTGAAATCAGAAATACAACTCGTGGATGATACACCAAAATTTAGTCATAAGA 939

Qy 729 GlySerSerAspGluAspAspGluAspGluHisIleGlyValPheSerGlnSer 748
Db 940 GAATCTGTTGAATCTTGACATCCACCTCGAGCTCCAGGAAATGGCTTTGGCTGGTTGTCT 999

Qy 749 PheLeuProAlaSerAspSerGluSerAspIleIlePheAspAsnGluAspGluAsnSer 768
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RESULT 4
US-09-799-875-18
; Sequence 18, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059

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940	GAATCTGGTGAACTTAGTCGACCGCTGGAGCTCCAGGAAAATGSCITTTGGCTGTGTTGTCT	999
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Db		
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? LOCATION: (114)...(2000)
US-09-799-875-16

Alignment Scores:
Pred. No.:      1.77e-37      Length:      2870
Score:          470.00        Matches:    161
Percent Similarity: 47.03%     Conservative: 69
Best local Similarity: 32.92%   Mismatches: 185
Query Match:      5.50%       Indels:     74
DB:               4           Gaps:       22

US-09-515-806A-2 (1-1649) x US-09-799-875-16 (1-2870)

QY 550 GlnSerProGluAspSerGlyGlyGlnAspTyrValGluThrValIleProSerAsnArg 569
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QY 590 PheGluGluLeuGlnLeuLeuGlyLysGlyAlaPheGlyAlaValIleLysValGlnAsn 609
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QY 610 LysLeuAspGlyCysCysTyrAlaValLysArgIleProIleAsnProAlaSerArgGln 629
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QY 630 Phe----ArgArgIleLysGlyGluValThrLeuLeuSerArgLeuHisHISgluAsnIle 648
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Db 732 GTTTCATGAAGTCTTCACGGGAAGTCAAGGTGCTGCCAGGTCTTCACACCCCCAATATT 791
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 649 ValArgTyrTyrAsnAlaTpIleGluArgHisGluArgProAlaGlyProGlyThrPro 668
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 792 GTTGCTATCACCGGTGGTAGAA--CATGTCATGTGATTCAGCCA-----839
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla--- 687
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 840 -----Lys-----CGAGACAGAGCTGCCATTGAGTTGCCATCTCTG 872
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QY 688 -----SerAspThrAsp 691
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Db 873 GAAGTGTCTCCGACCAGGAAGGACAGAGCAATGTGGTTTAAATAATGATCAAAGT 932
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 692 GlyLeuAspSerValGluAlaAlaProProProIleLeuSerSerVal---Glu 710
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 933 AGCAGCTCATCCATTATCTTGTCTGAGCCCACCCAGAAAAAGAAAAACGCTTTGGAGAA 992
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 711 TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 993 TCTGACATGAAATCAAGTAATCAAGTCGGTGAAGTACACCCACCAATTTAGTCATAAGA 1052
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 729 GlySerSerAspGluAspAspAspGluHisGlyValPheSerGlnSer 748
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1053 GNACTGGTGAACITGAGTCGACCCCTGGACTCCAGAAAAATGGCTGGCTGGTTTGCT 1112
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 749 PheLeuProAlaSerAspSerGluSerAspIleIlePheAspAsnGluAspGluAsnSer 768
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1113 -----GCCAGTTCAATTGTGGAACAGACAGCTCCCACTCAGCGCTAANTTCCACCTAGAG 1166
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1167 GAGAGTTTCACATCCACCGAAGAATCTCTCCGAAGAANAATGCACTTTTGGGTGAG--- 1223
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 789 SerValThrThruAlaValHistyr-----Leuty.rileGlnMetGluTyrCysGlu 806
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1224 -----ACAGGGCACAGTACCACTGATGCTGCATCATCGATGCGAGTGTGTGAG 1274
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1275 CTCTCGCTGTGGGATGGATAGTCGAGAGAAACAAGCGGGGGCGGAGGTATGTGCCAGG 1334
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

US-09-799-875-16
; Sequence 16, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 2870
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS

```

Y 817 GlyLeu-----TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp 834  
b 1335 TCTGCTGCTCTTATGTTATGGCAATGTTGCAACAAATATTTTCAAGAAATGGTAGAA 1394  
Y 835 GlyLeuAlaTyrIleHisGluLeuGlyMetIleHisArgAspLeuLysProValAsnIle 854  
b 1395 GGTGTGTTTACATACATAACATGGAATTTGTCACCGAGATCTGAAGCCCAAGAAATAT 1454  
Y 855 PheLeuAspSer---AspAspHisValIleGlyAspPheGlyLeuAla---ThrAsp 872  
b 1455 TTTCTTCATGCGCCCTGATCAGCAGTAAATATAGAGACTTTGCTGCGCTGCACAGAC 1514  
Y 873 HisLeuAlaPheSerAlaAspSerIysGlnAspGlnThrGlyAspLeuLysSer 892  
b 1515 ATCCCTA-----CAGAAGAACACACAGACTGGCAACCAACAGAAACCGGAAGAGA 1559  
Y 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGlu--- 911  
b 1560 ACACCAACA---CAT---ACGTCAGAGTGGTACTTCTGTACGCTTCACCCGACAG 1613  
Y 912 ValGlnGlySerThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIle 931  
b 1614 TTGGAAGGA-----TCTGAGTATGATGCCAAGTACAGATATGTACAGCTTGGGTGTG 1664  
Y 932 IlePhePheGluMetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeu 951  
b 1665 GTCCTGCTAGACTC---TTTCAGCCGTTTGGACACAGAAATGGAGCAGACAGATTCTA 1721  
Y 952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspGlyGluHis 971  
b 1722 ACAGGTTTAAAG-----ACTGGTCAGTTGCCGGAATCCCTCCGTAAA---AGGTGT 1769  
Y 972 AlaLysGlnLysSerValIleSerTripleLeuAsnHisAspProAlaLysArgProThr 991  
b 1770 CCGGTGCAAGCCCAAGTATATCCAGCACTTAACGAGAAGGAACTCATCGCAGACCATCT 1829  
Y 992 AlaThrGluLeuLeuLysSerGluLeu 1000  
b 1830 GCCATTCAGCTGCTGCAGAGTGAACCTT 1856

RESULT 6  
Sequence 1, Application US/09578441  
Patent No. 6562571  
GENERAL INFORMATION:  
APPLICANT: Wu, J.H. David  
APPLICANT: Omase, Takeshi  
APPLICANT: Mantalaris, Athanasios  
APPLICANT: Chen, Yi-Guang  
APPLICANT: Tsai, Ying-Chueh  
TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2, ALPHA KINASE  
FILE REFERENCE: 176/60571  
CURRENT APPLICATION NUMBER: US/09/578,441  
CURRENT FILING DATE: 2000-05-25  
PRIOR APPLICATION NUMBER: 60/135,713  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 1  
TYPE: DNA  
ORGANISM: Homo sapiens  
JS-09-578-441-1

Alignment Scores:  
Pred. No.: 1,79e-37 Length: 2891  
Score: 470.00 Matches: 161  
Percent Similarity: 47.03% Conservative: 69  
Best Local Similarity: 32.92% Mismatches: 185  
Query Match: 5.50% Indels: 74  
DB: 4 Gaps: 22

US-09-515-806A-2 (1-1649) x US-09-578-441-1 (1-2891)

QY 550 GlnSerProGluAspSerGlyGlyAspTyrValGluThrValIleProSerAsnArg 569  
Db 466 AGTCTCTGTTAAAGAGAGAGTTCGTGAGGATCCTTGTGAGGATATTTCTCGTATCCAGAA 525  
QY 570 LeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIleGlu 589  
Db 526 ATCAGATCAAGGAGTAGCTTGGAGCACAACT-----TCACGTTACTTAAATGAA 579  
QY 590 PheGluGluLeuGlnLeuGlyGlyGlyAlaPheGlyAlaValIleLysValGlnAsn 609  
Db 580 TTGGAAGAACTTGGCATCTTAGGAAAGAGTGGATACGGAAGAGTATACAGGTCAGGAAT 639  
QY 610 LysLeuAspGlyCysCysTyrAlaValIysArgIleProIleAsnProAlaSerArgGln 629  
Db 640 AAATTAGATGTTCACTATTATGCAATAAAAAAATCTCTGATTAAAGGTGCACTAAACCA 699  
QY 630 Phe---ArgArgIleLysGlyGluValThrLeuLeuSerArgIleHisGluAsnIle 648  
Db 700 GTTTCATGAAGAGTCTTACGGGAAGTGAAGGTGTCGCGAGTCTTCAGCACCCCAATATT 759  
QY 649 ValArgTyrTyrAsnAlaTrpIleGluArgHisGluArgProAlaGlyProGlyThrPro 668  
Db 760 GTTGGCTATCACACCGCTGGATAGAA---CATGTTCTATGATTCAGCCA----- 807  
QY 669 ProProAspSerGlyProLeuAlaLysAspAspArgAlaAlaArgGlyGlnProAla--- 887  
Db 808 -----CGAGACAGAGCTGCCATTGAGTTGCCCATCTCTG 840  
QY 688 -----SerAspThrAsp 691  
Db 841 GAAGTCTCTCCAGCAGGAAGAGCAGAGCAATGTTGTTTAAATAATGATGAAGT 900  
QY 692 GlyLeuAspSerValGluAlaAlaAlaProProIleLeuSerSerSerVal---Glu 710  
Db 901 ACAGCTCATCATTTATCTTCTGTCGACCCCAAGAAAGAAACCGCTTGGAGAA 960  
QY 711 TrpSerThrSerGlyGluArgSerAlaSerAlaArgPheProAla-----ThrGlyPro 728  
Db 961 TCTGACACTGAAATATCAGATAAACAAGTCGGTGAAGTACACCAACCAATTTAGTCATAAGA 1020  
QY 729 GlySerSerAspAspGluAspAspGluAspGluHisGlyGlyValPheSerGlnSer 748  
Db 1021 GAATCTGGTGAACCTTGAAGTCCAGCTCGAGCTCAGGAAATGGCTTGGCTGTTGCT 1080  
QY 749 PheLeuProAlaSerAspSerGluSerAspIlePheAspAsnGluAspGluAsnSer 768  
Db 1081 -----GCCAGTTCAATTTGGAACAGCAGCTGCCACTCAGGCGCTAATTCACACCTAGAG 1134  
QY 769 LysSerGlnAsnGlnAspGluAspCysAsnGluLysAsnGlyCysHisGluSerGluPro 788  
Db 1135 GAGAGTTTCACATCCACCAAGAAATCTTCGAGAAATGTCAACTTTTGGGTCAG--- 1191  
QY 789 SerValThrThrGluAlaValHisTyr-----LeuTyrIleGlnMetGluTyrCysGlu 806  
Db 1192 -----ACAGAGGCACAGTACCACTGATGTGTCACATCCAGATCCAGCTGTGTGAG 1242  
QY 807 LysSerThrLeu-----ArgAspThrIleAspGln 816  
Db 1243 CTCTCGTGTGGGATTGGATAGTTCGAGAGAAACAGCGCGCGCGAGTATGTGGACGAG 1302  
QY 817 GlyLeu-----TyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAsp 834  
Db 1303 TCTGCTGCTCTTATGTTATGGCCAATGTTGCAACAAAAATTTTCAAGAAATTTGGTAGAA 1362  
QY 835 GlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIle 854  
Db 1363 GGTGTGTTTACATACATACATCGGAATTTGTCACCGAGATCTGAAGCCCAAGAAATATT 1422  
QY 855 PheLeuAspSer---AspAspHisValIleGlyAspPheGlyLeuAla---ThrAsp 872  
Db 1423 TTTCTTCATGCGCCCTGATCAGCAAGTAAAAAATAGGAGACTTTGGTCTGCGCTGCACAGAC 1482

Y 873 HisLeuAlaPheSerAlaAspSerLysGlnAspGlnThrGlyAspLeuIleLysSer 892  
b 1483 ATCCTA-----CAGAGAACACAGACTGGACCAACAGAAACGGGAAGAGA 1527  
Y 893 AspProSerGlyHisLeuThrGlyMetValGlyThrAlaLeuTyValSerProGlu--- 911  
b 1528 ACACCAACA---CAT---ACGTCAGAGTGGTACTTCTGTACGCTTACCCGACAG 1581  
Y 912 ValGlnGlySerThrLysSerAlaTyrsnGlnLysValAspLeuPheSerLeuGlyIle 931  
b 1582 TTGGAAGGA-----TCTGAGTATGATCCCAAGTCAGATATGTACAGCTTGGGTGTG 1632  
Y 932 IlePhePheGluMetSerTyHisProMetValThrAlaSerGluArgIlePheValLeu 951  
b 1633 GTCTCTAGAGCTC---TTTCAGCGGTTTGGACAGAAATGGAGCCAGACAGATTCTA 1689  
Y 952 AsnGlnLeuArgAspProThrSerProLysPheProGluAspPheAspGlyGluHis 971  
b 1690 ACAGGTTTAAAGA-----ACTGGTCAGTGGCGGAATCCCTCCGTAAA---AGGTGT 1737  
Y 972 AlaLysGlnLysSerValIleSerTrpLeuLeuAsnHisAspProAlaLysArgProThr 991  
b 1738 CCAGTGCAGCAAGCAAGTATATCCAGCACTTAACGAGAGGAAGCACTATCGCAGACCATCT 1797  
Y 992 AlaThrGluLeuLysSerGluLeu 1000  
b 1798 GCATTTCAGTCTGCAGAGTGAATT 1824

## RESULT 7

US-09-016-434-785  
Sequence 785, Application US/09016434  
Patent No. 6500938  
GENERAL INFORMATION:  
APPLICANT: Janice Au-Young  
APPLICANT: Jeffrey J. Seilhamer  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
TITLE OF INVENTION: PATHWAY GENE EXPRESSION  
NUMBER OF SEQUENCES: 1490  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION NUMBER: US/09/016.434  
FILING DATE: HEREWITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
FILING DATE:  
APPLICATION NUMBER:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0002 US  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 785:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: HMT2AGT01

CLONE: 488190  
US-09-016-434-785  
Alignment Scores:  
Pred No.: 114e-36 Length: 244  
Score: 443.00 Matches: 81  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 5.18% Indels: 0  
DB: 4 Gaps: 0  
US-09-515-806A-2 (1-1649) x US-09-016-434-785 (1-244)  
QY 771 GlnAsnGlnAspClnAspCysAsnGlnLysAsnGlyCysHisGlnSerGluProSerVal 790  
Db 1 CAGATCAGATGAGATTCGCAATGAAAGAAATGCTCCCATGAAAGTGGACATCAGTG 60  
QY 791 ThrThrGluAlaValHisTyTrLeuTyTrIleGlnMetGluTyTrCysGluLysSerThrIeu 810  
Db 61 ACAGTACGGCTGTGCTACCTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACITTA 120  
QY 811 ArgAspThrIleAspClnGlyLeuTyTrArgAspThrValArgIleuTyTrArgLeuPheArg 830  
Db 121 CGAGACACCATTGACCGAGGACTGTATCGACACCGTCAGACTCTGGAGGCTTTTTCGA 180  
QY 831 GlnIleLeuAspGlyLeuAlaTyTrIleHisGlnLysGlyMetIleHisArgAspLeuLys 850  
Db 181 GAGATTCTGGATGGATTAGCTTATATCCATGAGAAAGAAATGATTCACCGGATTTGAAG 240  
QY 851 Pro 851  
Db 241 CCT 243

## RESULT 8

US-08-143-219-1  
Sequence 1, Application US/08143219  
Patent No. 5670330  
GENERAL INFORMATION:  
APPLICANT: Sorenberg, Mahum  
APPLICANT: Katze, Michael G.  
APPLICANT: Roy, Sophie  
APPLICANT: Koromilas, Antonis E.  
APPLICANT: Barber, Glen N.  
TITLE OF INVENTION: TUMOR-CELL ASSAY METHOD AND KIT  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: 611 West Sixth Street  
CITY: Los Angeles  
STATE: CA  
COUNTRY: USA  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM compatible  
OPERATING SYSTEM: PC-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/143.219  
FILING DATE: October 25, 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
PRIOR APPLICATION DATA: including application  
PRIOR APPLICATION DATA: described below:  
APPLICATION NUMBER: 08/141,244  
FILING DATE: October 22, 1993  
APPLICATION NUMBER: 07/953,681  
FILING DATE: September 29, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Douglas E. Olson  
REGISTRATION NUMBER: 22,798  
REFERENCE/DOCKET NUMBER: 204/139  
TELECOMMUNICATION INFORMATION:  
two

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2628 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
INDIVIDUAL ISOLATE: HUMAN PKR GENE, FIGURE 5  
FEATURE:

NAME/KEY: CDS  
LOCATION: 187..1836  
IS-08-143-219-1

Alignment Scores:  
Score: 5.55e-32  
Length: 2628  
Matches: 179  
Conservative: 87  
Percent Similarity: 37.10%  
Mismatches: 197  
Indels: 255  
Gaps: 31  
Query Match: 1

US-09-515-806A-2 (1-1649) x US-08-143-219-1 (1-2628)

329 GluLysGluLysIleAspLysCysLysGlnIleGlnGlyThrGluThrGluPheAsn 348  
344 CAGAAAGTGAAGGTAGATCAAGAGAGAGAGAA 376  
349 SerLeuValLysLeuSerHisProAsn---ValValArgTyrIleuAlaMetAsnLeuLys 367  
377 -----AAAATGCCGACCAAAATTACTGTTGAGATCTTAAAGGAAAGAGG 427  
368 GluGlnAspSerIleValValAspIleLeuValGluHisIleSer-----GlyVal 385  
428 CAG-----TTAGTCCTTTA-TTATTCACAACAACGAATCTTCAGAGGATTA 474  
386 SerLeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgTyr 405  
475 TCCATGGGGAATTACATAGGCCTTATCAATAGAAATTGCC-----CAGAGAAAGACTA 528  
406 ThrAla-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal 422  
529 ACTGTAATATTAGACAGTGTGCATCGGG-----GTGCATGGCCAGAGGATTT 579  
423 His----- 423  
580 CATTATAATGCAAAATGGGACAGAAAGATATAGTATTGTTACGTTCTACTAAACAG 639  
424 -----LysValLeuSerAlaSerAsnVal-----LeuValAspAlaGluGlyThr 438  
640 GAAGCAAAACAAATGGCGCTTAACTTCATATCTTCAGATATATCAGAGAAACCTCA 699  
439 ValLysIleThrAspTyrSerIleSerIleArgLeuAlaAspIleCysLysGluAspVal 458  
700 GTGAAA---TCTGACTACCTGCTCTGTTTCTGTTTCTGTTTCTGTTGAGTCC----- 750  
459 PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys 478  
751 -----CAAGCAACTCTTTAGTGACCAGCACA----- 777  
479 GlyAspValTrpArgLeuGluLeuLeuSerLeuSerGlnGlnGluCysGly 498  
778 -----CTCGCTTCTGAATCATCATCTCAAGGT----- 804  
499 GluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysLys 518  
805 -----GACTTCTCAGCAGATACATCAGAGATAATCTAC--- 837  
519 CysValCysLeuAspAspLysGluArgTrpSerProGlnGlnLeuLysHisSerPhe 538

838 -----AGTGACAGTTTAAACAGTCTCTCGTTGCTTATGATGCTCTC 879  
539 IleAsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGln 558  
880 AGAAATAATCAAGAGAGGCAAAA----- 903  
559 AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGlu 578  
904 -----AGATCTTTGGCCACCAGATTGACCTTCTCTGAC-----ATCAAGAA 945  
579 ThrGlnArgGlnPheSerArgTyrPhe---IleGluPheGluGluLeuGlnLeuGly 597  
946 ACAAGTATCTGTGGACAAGAGGTTTGGCATGATTTAAAGAAATAGAAATTAATTGGC 1005  
598 LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAla 617  
1006 TCAGGTGATTTGGCCAAAGTTTCAAGCAAAACACAGAAATTGACGGAAGAACTTACGTT 1065  
618 ValLysArgIleProIleAsnProAlaSerArgGlnPheArgArgIleLysGlyGluVal 637  
1066 ATTAACGTTTAAATATATAAC-----GAGAAGCGGAGCGTGAAGTA 1110  
638 ThrLeuLeuSerArgLeuHisGlnLysIleValArgTyrTyrAsnAlaTrpIleGlu 657  
1111 AAAGCATTGGCAAACTTGATCATGATAAATATTGTTCACTACAAATGGCTGTGG----- 1164  
658 ArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLys 677  
1164 ----- 1164  
678 AspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGlu 697  
1165 -----GATGATTGAT----- 1176  
698 AlaAlaProProIleLeuSerSerValGluTrpSerThrSerGlyGluArg 717  
1176 ----- 1176  
718 SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGluAspAsp 737  
1177 -----TATGATCTGAGACCAAAAATAGTTCAAG----- 1203  
738 GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer 757  
1204 -----CTTGAGAGCAGT----- 1215  
758 AspIlePheAspAsnGluAspGluAsnSerLysSerGlnAsnGlnAspGluAspCys 777  
1216 -----GATTATGATCTGAGAACACCAAAAATAGTTCAAG----- 1251  
778 AsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAlaValHisTyr 797  
1252 ---TCAAAGACTAAGTGC----- 1266  
798 LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp----- 815  
1267 CTTTTCATCCAAATGGATCTCTGATAAAGGACCTTGGAAACATGGATTGAAAAAGA 1326  
816 GlnGlyLeuTyrArgAspThrValArgLeuTrpArgLeuPheArgGluIleLeuAspGly 835  
1327 AGAGCGGAGAAACTAGACAAAGTTTGGCTTTGGAACTCTTTGAAACAAATAACAAAGGG 1386  
836 LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe 855  
1387 GTGATTTATATATTCACAAAAAATAATTATTCATAGATCTTAAGCCAAAGTAATATATTC 1446  
856 LeuAspSerAspAspHisValLysIleGlyAspPheGlyLeuAlaThrAspHisLeuAla 875  
1447 TTAGATACAAACCAAGTAAAGATTGGAGACTTTGGACTTTGTAACTCT----- 1497  
876 PheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSerAspProSer 895



1438	----	CTGAAAATGAT-----	1509
896	GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer	915	
1510	CGAAAGCGAAACAAGGAGTAAGGAACTTTGCGATACATGAGCCACAGACATTTCTTCG	1569	
916	ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIlelelaphPheGlu	935	
1570	-----CAAGACTATGAAAGAGTGGACCTCTACGCTTTGGGCTAATTCTTGCTGAA	1623	
936	MetSerTyrHisProMetValThrAlaSerGluA-GIlePheValLeuAsnGlnLeuArg	955	
1624	CTT---CTTCATGTATGTGCATCTGCTTTGAAACATCAAACTTTTTCACAGACCTACGG	1680	
956	AspProThrSerProLysPheProGluAspPheAspAspGlyGluHisAlaLysGlnLys	975	
1681	GATGCATC-----ATCTCAGATATATTTGAT-----AAAAAGAAAAA	1719	
976	SerValIleSerTyrProLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu	995	
1720	ACTCTTCTACAGAAATTACTCTCAAGAAACCTGAGATCGACCTPAACACATCTGAATA	1779	
996	LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis	1012	
1780	CTAAGGACCTTGACTGTGTGGAGAAAAGCCACAGAAAAATCAACGCAC	1830	

Pred. No.:	9.59e-32	Length:	2562
Score:	413.50	Matches:	179
Percent Similarity:	37.10%	Conservative:	87
Best Local Similarity:	24.97%	Mismatches:	198
Query Match:	4.84%	Indels:	254
DB:	2	Gaps:	31

US-09-515-806A-2 (1-1649) x US-08-436-771-8 (1-2562)

Qy	329	GluLysGluLysIleAspLysCysLysGlnIleGlnGlyThrGluThrGluPheAsn	348
Db	344	CAGAAGGTGAAGGTAGATCAAGAAGGAAGCAA	376
Qy	349	SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys	367
Db	377	-----AAAATGCCACCCAAATAGCTGTGAGATACITTAAGGAAAGAAAGAG	427
Qy	368	GluGlnAspAspSerIleValValAspIleLeuValGluHisIleSer	385
Db	428	CAG-----TTAGTCCCTTTA-TTATTGACAAACAGAAATCTTTCAGAAAGATTA	474
Qy	386	SerLeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgGlyTyr	405
Db	475	TCCATGGGGAATTACATAGGCGCTTATCAATAGATTGCC-----CAGAAGAAAGACTA	528
Qy	406	ThrAla-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal	422
Db	529	ACTGTAATTAATGAACAGTGTGCATCGGG-----GTGCATGGCCAGAAAGATT	579
Qy	423	His-----	423
Db	580	CATTATAATGCAAAATGGGACAGAAAGATATAGTATTGGTACAGGTCTACTAAACAG	639
Qy	424	-----LysValLeuSerAlaSerAsnVal-----LeuValAspAlaGluGlyThr	438
Db	640	GAAGCAAAACAATTGGCGCTAAACTTGCATATCTTCAGATATTATCAGAAGAAAGACTCA	699
Qy	439	ValLysIleThrAsnTyrSerIleSerLysArgLeuAlaAspIleCysLysGluAspVal	458
Db	700	GTGAAA---CTGACTACTGTGCTCTGGTCTTTTCTTACTAGGTGAGTCC-----	750
Qy	459	PheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys	478
Db	751	-----CAAAGCAACTCTTTAGTGACCAACACA-----	777
Qy	479	GlyAspValTrpArgLeuGlyLeuLeuLeuSerLeuSerGlnGlyGlnGluCysGly	498
Db	778	-----CTCGCTTCTGAAATCATCATCTGHAAGT-----	804
Qy	499	GluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysLys	518
Db	805	-----GACTTCTCAGCAGATACATCAGAGATA-----	831
Qy	519	CysValCysLeuAspAspLysGluArgTrpSerProGlnLeuLeuLysHisSerPhe	538
Db	832	-----AATCTTAACAGTGACAGTTTAACACAGTCTTCGTGCTTATGATGTGCTC	892
Qy	539	IleAsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGln	558
Db	883	AGAAATAATCAAGGAGCGCAAAA-----	906
Qy	559	AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGlu	578
Db	907	-----AGATCTTTGGCACCCAGATTTGCACCTTCTGTAC-----ATGAAAGAA	948
Qy	579	ThrGlnArgGlnPheSerArgTyrPhe---IleGluPheGluGluLeuGlnLeuLeuGly	597
Db	949	ACAAGTATACTGTGCACAGAGGTTTGGCATGGATTTTAAAGAAATAGAAATTAATTGGC	100
Qy	598	LysGlyAlaPheClyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAla	617
Db	1009	TCAGGTGGATTTGGCCAAAGTTTCAAGCAAAACACAGAATTTCACGGAAGACTTACGTT	106

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678 AspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGlu 697  
1168 -----GATGGATTGTAT----- 1179  
698 AlaAlaProProIleLeuSerSerValGluTrpSerThrSerGlyGluArg 717  
1179 ----- 1179  
718 SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGluAspAsp 737  
1180 -----TATGATCCTGAGACCATGATGATCT----- 1206  
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1207 -----CTTGAGAGCACT----- 1218  
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1255 -----TCAAGACATAAGTGC----- 1269  
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1513 CGAAAGCGCAACAGAGTAGGGGAACCTTTCGATACATGAGCCCGAGACAGATTTCTTCG 1572  
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Db 1723 ACTCTTCTACGAATAATTACTCTCAAGAAACCTGAGATCGACCTACACATCTGAATA 1782  
Qy 996 LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012  
Db 1783 CTAAGACCTTGACTGTGTGGAAGAAAGCCAGAGAAATAATGAACGACAC 1833  
RESULT 10  
US-08-434-998-8  
; Sequence 8, Application US/08434998  
; Patent No. 5866781  
; GENERAL INFORMATION:  
; APPLICANT: Silverman, Robert H.  
; APPLICANT: Sengupta, Dibyendu N.  
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,  
; TITLE OF INVENTION: Cells and Methods  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rudett, Barnett, McClosky, Smith, Schuster &  
; STREET: 200 E. Broward Boulevard  
; CITY: Fort Lauderdale  
; STATE: Florida  
; COUNTRY: USA  
; ZIP: 33301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/434,998  
; FILING DATE:  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/198,973  
; FILING DATE: 18-FEB-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Manso, Peter J.  
; REGISTRATION NUMBER: 32,264  
; REFERENCE/DOCKET NUMBER: CL11363-16  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 305/527/2498  
; TELEFAX: 305/764/4996  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2562 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-08-434-998-8  
Alignment Scores:  
Pred. No.: 9,59e-32 Length: 2562  
Score: 413.50 Matches: 179  
Percent Similarity: 37.10% Conservative: 87  
Best Local Similarity: 24.97% Mismatches: 198  
Query Match: 4.84% Indels: 254  
DB: 2 Gaps: 31  
US-09-515-806A-2 (1-1649) x US-08-434-998-8 (1-2562)  
Qy 329 GluLysGluLysIleAspLysCysLysLysGlnIleGlnGlyThrGluThrGluPheAsn 348  
Db 344 CAGAAGTGAAGGTAGTATCAAGAGAGGAGCA----- 376  
Qy 349 SerLeuValLysLeuSerHisProAsn---ValValArgTyrIleAlaMetAsnLeuLys 367  
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Qy 368 GluGlnAspAspSerIleValValAspIleLeuValGluHisIleSer-----GlyVal 385

428 CAG-----TTAGTCCCTTTA-TTATTGACAAACAAAGATTCTTCAGAAAGATT 474  
386 SerLeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgArgTyr 405  
475 TCCATGGGAATTACATAGCCCTTATCAATAGAAATTGCC-----CAGAAGAAAGACTA 528  
406 ThrAla-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal 422  
529 ACTGTAAATTATGAACAGCTGTGCATCGGG-----GTGCATGGCCAGAAAGATT 579  
423 His-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal 422  
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559 AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPhePheSerGlu 578  
907 -----AGATCTTTGGCCACCAGATTGACCTCTCTGAC-----ATGAAAGAA 948  
579 ThrGlnArgGlnPheSerArgTyrPhe-----IleGluPheGluGluLeuGlnLeuGly 597  
949 ACAAGTATATCTGGCAAGAGCTTTGGCATGGATTAAAGAAATAGAAATTAATTGCC 1008  
598 LysGlyAlaPheGlyAlaValIleLysValGlnAsnLysLeuAspGlyCysCysTyrAla 617  
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618 ValIysArgIleProIleAsnProAlaSerArgGlnPheArgArgIleLysGlyGluVal 637  
1069 ATTAAACGTGTTAAATATATAAC-----CAGAAGCGGAGCGCTGAAGTA 1113  
638 ThrLeuLeuSerArgLeuHisGlnAsnIleValArgTyrTyrAsnAlaIleThrIleGlu 657  
1114 AAAGCATTTGGCAAACTTGATCATGTAAATATTGTTCACTACAATGCTCTG----- 1167  
658 ArgHisGluArgProAlaGlyProGlyThrProProAspSerGlyProLeuAlaLys 677  
1167 ----- 1167  
678 AspAspArgAlaAlaArgGlyGlnProAlaSerAspThrAspGlyLeuAspSerValGlu 697  
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698 AlaAlaAlaProProIleLeuSerSerSerValGluTyrSerThrSerGlyGluArg 717  
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Qy 718 SerAlaSerAlaArgPheProAlaThrGlyProGlySerSerAspAspGluAspAsp 737  
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Qy 738 GluAspGluHisGlyGlyValPheSerGlnSerPheLeuProAlaSerAspSerGluSer 757  
Db 1207 -----CTTGAGAGCAGT----- 1218  
Qy 758 AspIlePheAspAsnGluAspGluAsnSerLysSerGlnAsnGlnAspGluAspCys 777  
Db 1219 -----GATTATGATCCTGAGACACAAATAATAGTTCAAG----- 1254  
Qy 778 AsnGluLysAsnGlyCysHisGluSerGluProSerValThrThrGluAlaValHisTyr 797  
Db 1255 -----TCAAGACTAAGTGC----- 1269  
Qy 798 LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp----- 815  
Db 1270 CTTTTCATCAAAATGGAATCTGTGATAAAGGAGCCTTGGAAACAATGGAATGGAAGAA 1329  
Qy 816 GlnGlyLeuTyrArgAspThrValArgLeuTyrArgLeuPheArgGluLeuLeuAspGly 835  
Db 1330 AGAGCGCAGAACTAGACAAAGTTTGGCTTTGGACCTTTTGAACAATAACAAAGGG 1389  
Qy 836 LeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysProValAsnIlePhe 855  
Db 1390 GTGGATTATATACATTCAAAATAATTAATTCATAGAGATCTTAAGCCAAGTAATATATTC 1449  
Qy 856 LeuAspSerAspAspHisValIleGlyAspPheGlyLeuAlaThrAspHisLeuAla 875  
Db 1450 TTAGTAGATCAAAACAAGTAAGATGGAGACTTTGGACTTTGTACATCT----- 1500  
Qy 876 PheSerAlaAspSerLysGlnAspAspGlnThrGlyAspLeuIleLysSerAspProser 895  
Db 1501 -----CTGAAAAATCAT----- 1512  
Qy 896 GlyHisLeuThrGlyMetValGlyThrAlaLeuTyrValSerProGluValGlnGlySer 915  
Db 1513 GGAAGCGAAACAGAGTAGAGGAACTTTGCCATCATACAGCCAGAACAGATTTCTTCG 1572  
Qy 916 ThrLysSerAlaTyrAsnGlnLysValAspLeuPheSerLeuGlyIleIlePheGlu 935  
Db 1573 -----CAAGACTATGGAAGGAGTGGACCTTACGCTTTGGGCTAATTTCTGCTGA 1626  
Qy 936 MetSerTyrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955  
Db 1627 CTT---CTTCATGTATGTGACACTGCTTTTGAACAATCAAAAGTTTTCACAGCCTACGG 1683  
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Db 1684 GATGGCATC-----ATCTCAGATATATTGAT-----AAAAAGAAAA 1722  
Qy 976 SerValIleSerTyrLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995  
Db 1723 ACTCTCTACAGAAATTTACTCTCAAGAAACCTGAGGATCGACCTAACACATCTGAATA 1782  
Qy 996 LeuLysSerGluLeuLeuProProGlnMetGluSerGluLeuHis 1012  
Db 1783 CTAAGGACCTTGACTGTGTGGAAGAAAGCCAGAGAAATAATGACGACAC 1833

RESULT 11  
US-08-487-797-8  
; Sequence 8, Application US/08487797  
; Patent No. 5866787  
; GENERAL INFORMATION:  
; APPLICANT: Silverman, Robert H.  
; APPLICANT: Sengupta, Dibyendu N.  
; TITLE OF INVENTION: Transgenic Plants Co-Expressing A  
; TITLE OF INVENTION: Functional Human 2-5A System  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Holland & Knight

STREET: One E. Broward Boulevard, #1300  
 CITY: Fort Lauderdale  
 STATE: Florida  
 COUNTRY: USA  
 ZIP: 33301  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION INFORMATION:  
 APPLICATION NUMBER: US/08/487,797  
 FILING DATE: 07-JUNE-1995  
 CLASSIFICATION: 800  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Manso, Peter J.  
 REGISTRATION NUMBER: 32,264  
 REFERENCE/DOCKET NUMBER: CL11363-16(C)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 305/468-7811  
 TELEFAX: 305/463-2030  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2562 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 JS-08-487-797-8

Alignment Scores:  
 Pred. No.: 9 59e-32 Length: 2562  
 Score: 413.50 Matches: 179  
 Percent Similarity: 37.10% Conservative: 87  
 Best Local Similarity: 24.97% Mismatches: 198  
 Query Match: 4.84% Indels: 254  
 DB: 2 Gaps: 31

JS-09-515-806a-2 (1-1649) x US-08-487-797-8 (1-2562)

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 Db 344 CAGAGGTGAAGTAGATCAAGAGGAAAGCAAA 376  
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 Db 1255 -----TCAAAAGACTAAGTGC----- 1269  
 Qy 798 LeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspThrIleAsp----- 815  
 Db 1270 CTTTTCATCAAAATGGAATCTCTGATATAAGGACCTTGGAAACAATGGATGAAAGAA 1329  
 Qy 816 GluGlyLeuTyrArgAspThrValArgLeuTyrPheArgLeuGluLeuLeuAspGly 835

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b 1390 GTGGATTATATACATTCAAAAAATTAATTCATAGAGATCTTAAGCCAAAGTAATATATTC 1449  
y 856 LeuAspSerAspHisValLysIleGlyAspPheGlyLeuAlaThrAspHisLeuAla 875  
b 1450 TTAGTAGATACAAAACAAAGTAAGATGGAGACTTTGGACTTTGTAACATCT- 1500  
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b 1573 -----CAAGACTATGGAAGGAGTAGGACCTACGCTTTGGGCTAATCTTCTGAA 1626  
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b 1627 CTT---CTTCATGTATGTGACACTGCTTTTGAACACATCAAAAGTTTTCACAGACCTACGG 1683  
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b 1684 GATGGCATC-----ATCTCAGATATATTTGAT-----AAAAAGAA 1722  
y 976 SerValLysSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995  
b 1723 ACTCTTCTACAGAAATTAATCTCTCAAGAAACCTGAGGATCGACCTAACACATCTGAATA 1782  
y 996 LeuLysSerGluLeuLeuProProGlnMetGluLysSerGluLeuHis 1012  
b 1783 CTAAGGACCTTGACTGTGTGAAGAAAGCCAGAGAAATGAGACAC 1833

RESULT 12

Sequence 8: Application PC/TUS9502058  
GENERAL INFORMATION:  
APPLICANT: Silverman, Robert H.  
TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,  
TITLE OF INVENTION: Cells and Methods  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
ADDRESS: Russell  
STREET: 200 E. Broward Boulevard  
CITY: Fort Lauderdale  
STATE: Florida  
COUNTRY: USA  
ZIP: 33301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/02058  
FILING DATE:  
CLASSIFICATION:  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US 08/198,973  
FILING DATE: 18-FEB-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Manso, Peter J.  
REGISTRATION NUMBER: 32,264  
REFERENCE/DOCKET NUMBER: CL11363-16  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 305/527/2498

TELEFAX: 305/764/4996  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2562 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US95-02058-8  
Alignment Scores:  
Pred. No.: 9,598-32 Length: 2562  
Score: 413.50 Matches: 179  
Percent Similarity: 37.10% Conservative: 87  
Best Local Similarity: 24.97% Mismatches: 198  
Query Match: 4.84% Indels: 254  
DB: 5 Gaps: 31  
US-09-515-806A-2 (1-1649) x PCT-US95-02058-8 (1-2562)  
Qy 329 GluLysGluLysIleAspLysCysLysLysGlnIleGlnGlyThrGluThrGluPheAsn 348  
Db 344 CAGAAGGTGAAGGTAGATCAAAAGAAAGGAAGCAA----- 376  
Qy 349 SerLeuValLysLeuSerHisProAsn---ValValArgTyrLeuAlaMetAsnLeuLys 367  
Db 377 -----AAATGCCCGCAGCCAAATAGCTGTTCAGATATCTTAATAGGAAAGAGG 427  
Qy 368 GluGlnAspSerIleValValAspIleLeuValGluHisIleSer-----GlyVal 385  
Db 428 CAG-----TTAGTCTTTA-TTATTGACAAACAAAGATTTCTTCAGAGGATTA 474  
Qy 386 SerLeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgTyr 405  
Db 475 TCCATGGGAATTTACATAGCCCTTATCAATGAATGGC-----CAGAAGAAAGACTA 528  
Qy 406 ThrAla-----GlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValVal 422  
Db 529 ACTGTAAATTTACACAGTGTGCATCGGG-----GTGCATGGGCCAGAGGATTT 579  
Qy 423 His----- 423  
Db 580 CATTATAAATGCAAAATGGGACAGAAAGAAATATAGTATTGGTACAGGTTCTACTAAACAG 639  
Qy 424 -----LysValLeuSerAlaSerAsnVal-----LeuValAspAlaGluGlyThr 438  
Db 640 GAAGCAAAACAAATGGCCGCTAACTGCATATCTTCAGATATTTATCAGAGAAACCTCA 699  
Qy 439 ValLysIleThrAspTyrSerIleSerLysArgLeuAlaAspIleCysLysGluAspVal 458  
Db 700 GTGAAA---TCTGACTACCTGCTCTCTGTTCTTTGCTACTACTACGTGTGAGTCC----- 750  
Qy 459 PheGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLysLys 478  
Db 751 -----CAAAGCACTCTTTAGTACCCAGCACA----- 777  
Qy 479 GlyAspValTrpArgLeuGlyLeuLeuLeuSerLeuSerGlnGlyGlnGlyCysGly 498  
Db 778 -----CTCGCTTCTGAATCATCATCTGAAGGT----- 804  
Qy 499 GluTyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysLys 518  
Db 805 -----GACTTCTCAGCAGATACATCAGAGATA----- 831  
Qy 519 CysValCysLeuAspAspLysGluArgTrpSerProGlnGlnLeuLysHisSerPhe 538  
Db 832 -----AATTCTAACAGTACAGTCTTAACACAGTCTTCGTTGTTGTTATGATGCTC 882  
Qy 539 IleAsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGlyGln 558  
Db 883 AGAAATAATCAAGGAAGGCAAAA----- 906  
Qy 559 AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAlaPheSerGlu 578

**D**b     **B**d     **C**t     **G**a     **T**c  
1573 -----CAAGACATGCGAAGAAGTGGACCCTCATTGTTCCTTTGGGGTGTAATCTTCTGTGA 1626

**Q**y     936 MetSerThrHisProMetValThrAlaSerGluArgIlePheValLeuAsnGlnLeuArg 955  
      ::                |||||            |||  
**D**b     1627 CTT---CTTGCATGTACTGACACTGCTTTGAACAATCAAAGTTTTTCACACCTAACGCCG 1683  
                  |||||

**Q**y     956 AspProThrSerProLysPheProGluAspPheAspGlyGluHisAlaLysGlnLys 975  
      ::                |||||            |||  
**D**b     1684 CATGCCATC-----ATCTCAGATAATTATTGAT-----AAAAAAGAAA 1722

**Q**y     976 SerValleSerTrpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeu 995  
      ::::::::::                |||||            |||  
**D**b     1723 ACTCTTCTCACAGAAATTAATCTCTCAAGAAAACCTGAGCATCCGACTAACACATCTGAAATA 1782

**Q**y     996 LeuLysSerGluLeuLeuProProGlnMetGluGluSerGluLeuHis 1012  
      ::::::::::                |||||            |||  
**D**b     1783 CTAAAGACCTTGACTGTGTGGAGAAAAGCCCAGAGAAAATGAACGACAC 1833

**R**ESULT 13  
US-09-554-726A-11 ; Sequence 11, Application US/09554726A  
; Patent No. 6642369  
; GENERAL INFORMATION:  
; APPLICANT: HERENANN, Bernhard  
; APPLICANT: KOSCHORZ, Birgit  
; TITLE OF INVENTION: NUCLEIC ACIDS INVOLVED IN THE RESPONDER PHENOTYPE AND APPLICATION;  
; FILE REFERENCE: 258.0009.0101  
; CURRENT APPLICATION NUMBER: US/09/554,726A  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: PCT/EP 98/07395  
; PRIOR FILING DATE: 1998-11-18  
; PRIOR APPLICATION NUMBER: EP 98 10 3596.7  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: EP 97 12 0190.0  
; PRIOR FILING DATE: 1997-11-18  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: Patentin version 3.1  
SEQ ID NO 11  
TYPE: DNA  
LENGTH: 2827  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (524)..(1975)  
OTHER INFORMATION:

US-09-554-726A-11

Alignment Scores:

Pred. No.:	Score:
6_06e-26	Length: 2827
358.00	Matches: 185
Percent Similarity:	Conservative: 123
Best Local Similarity:	Mismatches: 254
Query Match:	Indels: 212
DB:	Gaps: 35

US-09-515-806A-2 (1-1649) x US-09-554-726A-11 (1-2827)

**Q**y     345 ThrGluPheAsenSerLeuValLysLeuSerHisProAsnValValArgTyrrLeu--Ala 363  
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**D**b     674 TCTGAGCGCAGCTTACTGATGATCACCATCCGATATCATCTCTCTCTTCAAGTC 733  
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**Q**y     364 MetAsnLeuLysGluGlnAspSerrileValValAspileLeuValGluHiseSer 383  
      :::                |||||            |||  
**D**b     734 ATGAGACCCAGAGAAA-----GTATACCTCATATTGAGTTGTGGAG 778

**Q**y     384 GlyvalserLeualaahisLeuSerHisSerGlyProfileProValHisGlnLeuArg 403  
      :::                |||||            |||  
**D**b     779 GGTAAATCACTTTACCAACACATCCAATACTGGTACCTGCAGAGGAGTAGAAGCAGC 838  
                  |||||

**Q**y     404 ArgTyrrThrAlacglnLeuSerGlyLeuasptyrrLeuHisSerAsnSerValValHis 423  
      :::                |||||            |||

839 CCATTATTCAGCAGCTCTTAAGTGTATGAACCTACTCTGCCAACACCGGGTATAGTTAC 898  
424 LysValLeuSerAlaSerAsnValLeuValLeuAlaAspAlaGluGlyThrValLysIleThrAsp 443  
899 AGGACCTGACACCTGACATATATGCTAGAAAAGATGGAAAGTGAAGATCATTCAT 958  
444 TyrSerIleSerLysArgLeuAlaAsp-----IleCysLysGluAsp 457  
959 TTGGACTCTGGCACCAGAGAACAGCAGGCAACCACTATTCTGTGAGATTATC 1018  
458 ValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyrLysThrGlyLys 477  
1019 CCATTAGTACTCTGAGGTGCTCTTTAAC-----AGACCTATGATATG---GCG 1066  
478 LysGlyAspValTrpArgLeuGlyLeuLeuLeuLeuSerLeuSerClnGly----- 494  
1067 AAGATCATGTGTGGGTCTGTGGAGTTGTCTGTATTTATGTGTAACTGGAAGATTCTG 1126  
495 -----GlnGluCysGlyGlu 499  
1127 TTTGATACTGCCAGCTAGAAAAGCTGCGAAACAAATGTTGTCAGAAAAGTGT----- 1180  
500 TyrProValThrIleProSerAspLeuProAlaAspPheGlnAspPheLeuLysCys 519  
1181 -----TCTGTCTCCCTGAGACTGTCTAGTAGAGCTCCAGACCTGATTAGACTTTTA 1231  
520 ValCysLeuAspAspLysGluArgTrpSerProGlnGlnLeuLeuLysHisSerPheIle 539  
1232 ATGACGGACATCCCGCACTTAGCCCACTGTGCTGAGTTATGTGATCCCTGGTGC 1291  
540 AsnProGlnProLysMetProLeuValGluGlnSerProGluAspSerGlyGly---Gln 558  
1292 ACA-----GAAGCTCAGGGGTGTATACCA 1315  
559 AspTyrValGluThrValIleProSerAsnArgLeuProSerAlaAla----- 574  
1316 GATCTTGTGAAGAACATATACCTCAAGCCAGACCTCGGATTCGAAAGCAATGGGA 1375  
575 PhePhe-----SerGluThrGlnArgGlnPheSerArg 585  
1376 TTTATCGGGTTCAGAGCTCAAGACATTCGAAGATTCGTTATGTGAGAGAAAATTCACGAA 1435  
586 TyrPheIleGluPheGluGluGluGlnLeuLeuGlyLysGlyAlaPheGlyAlaValIle 605  
1436 ACCATGGCATCTTAT-----TGTCTACTG 1459  
606 LysValGlnAsnLysLeuAspGlyCysTyrAlaValLysArgIleProIleAsnPro 625  
1460 AAAAAACAG---ATTCTTAAGGAATGTACAGGCCAATCCGGGCTCAGCCCATGAATCCA 1516  
626 AlaSerArgGln-----PheArgArg 632  
1517 TCTGTGACCCCACTCTCTCCCTTGTGATGCTCCTACTTCCATCTCGGACTTCGGAGG 1576  
633 IleLysGlyGluValThrLeuLeuSerArgLeuHisGluAsnIleValArgTyrTyr 652  
1577 ACAGAGACTGAACCCACACAGGCTCAGATTATCTGACAAATAAGGAAGTCCCTGTGTGGC 1636  
653 AsnAlaTrpIleGluArgHisGluArgPro---AlaGlyProGlyThrProProAsp 671  
1637 AATAGTACTAGTAAGAAAAGAGAGAGAGATTTCAGTGGCGCGGT----- 1681  
672 SerGlyProLeuAlaLysAspArgAlaAlaArgGlyGlnProAlaSerAspThrAsp 691  
1682 -----GTTCTCAGCGCCGATTACACACACACCC 1711  
692 GlyLeuAspSerValGluAlaAla-----AlaProProIleLeuSer----- 706  
1712 ACAATGGACCAACACACACCCGTAAGTGGAGTGTGCTCCCTGCAATTTACTCAAATGTTTC 1771  
707 -----SerSerValGlnTrpSerThrSerGlyGluArgSerAlaSerAla-Arg 722  
1772 ACATCCATCCAAACAGCATCAATGAGAGTACAGAGGCCACATCATGTAACCTCAGCAGAG 1831

QY 722 gPheProAlaThrGlyProGlySerSerAspAspGluAspAspGluAspGluHisG1 742  
Db 1832 GATA-----AGCCTGTCACAGCAGAGCTGCCACAGAGGCATCAAGGGC 1876  
QY 742 yGlyValPheSer-----GlnSerPheLeuProAlaSerAspSerGluSe 757  
Db 1877 TGGACTAGGAAGATAGAAATGCAATGAGGAAGCTCTCTGTGTATCCCATCCAAAGAG 1936  
QY 757 rAspIleIlePheAspAsnGluAspGluAsnSerLysSerGlnAsnGlnAspGluAspCy 777  
Db 1937 ACATCTCACCTGGGCGAGAGAAGAGTCTGCCCAAAAATTTAAGACACAGGAA----- 1988  
QY 777 sAsnGluLysAsnGlyCysHisGluSerGlu-----ProSerValThr-ThrG 793  
Db 1989 -----GGATGTCAGAGAAATGAGCATCCAGCATGGCCCGCAGCTTTCAGACCG 2035  
QY 793 luAlaValHisTyrLeuTyrIleGlnMetGluTyrCysGluLysSerThrLeuArgAspT 813  
Db 2036 AAGGC-----AAGCTCTACTCTGATCTCTCGGGGAGGTGACCTCTTCACCA 2089  
QY 813 hrIleAspGlnGlyLeuTyr-----ArgAspThrValArgLeuTrpArgLeuPheArgG 831  
Db 2090 GGCTTTCCAAAGAGGTGATGTTTCACGGAGGAGGATGTCAAGTTCTAC-----CTGGCTG 2143  
QY 831 luIleLeuAspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLysP 851  
Db 2144 AGCTGGCTTGGCTCTAGACCACCTCCATGGCTGGGATCATCTACAGGGATCTGAAGC 2203  
QY 851 roValAsnIlePheLeuAspSerAspHisValLysIleGlyAspPheGlyLeu----- 869  
Db 2204 CAGAGATATCTCTCGATGATGAAGGGACATATTAAGATCAGATTTTGGCTTGAGCA 2263  
QY 870 -----AlaThrAspHis-----LeuAlaPheSerAlaAspSerLysGlnAspAspGlnT 886  
Db 2264 AGGAGGCCACCGACCATGACAGAGAGCCTATTCA----- 2298  
QY 886 hrGlyAspLeuIleLysSerAspProSerGlyHisLeuThrGlyMetValGlyThrAlaL 906  
Db 2299 -----TTTTGTGGGACTATTG 2314  
QY 906 eutyValSerProGluVal-----GlnGlySerThrLysSerAlaTyrAsnGlnL 923  
Db 2315 AATACATGGCGCCGAGGTGGTGAACCGCGGTGACACACACAGAGTGCC----- 2364  
QY 923 ysValAspLeuPheSerLeuGlyIlePhePheGluMetSerTyrHisProMetValT 943  
Db 2365 -----GACTGGTGGTCTTCGGTGTGCTCATGTTCCAGATGCT-CAC----- 2405  
QY 943 hrAlaSerGluArgIlePheValLeuAsnGlnLeuArgAspProThrSerProLysPheP 963  
Db 2406 -----AGGTCCTCGCCATTCACAGGGGAAG 2430  
QY 963 roGluAspPheAspAspGlyGluHisAlaLysGlnLys-----SerValIleSerT 980  
Db 2431 GACAGGAAGAAACAATGGCCCGCATCTCTCAAGCAAGCTGGGTATGCTTAGTTCTCTC 2490  
QY 980 rpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeuLeuLys----- 997  
Db 2491 AGTGGGAGGCTCAGACCTGCTCAGGGCCCTTTTCAAGCGGAACCCCTGCAACCGGCTA 2550  
QY 998 -----SerGluLeuLeuProProGlnMetGluGluSerGluHisGlu---V 1014  
Db 2551 GGTAAGGTCTCCT-GTGACACACCCCCACCCAG-----GAATGCAATGAGGCTG 2597  
QY 1014 alLeuHisHisThrLeuThrAsnValAspGly 1024  
Db 2598 CCTCTAGACCCCTTAGGAATGTGAGAGGC 2629

RESULT 14  
US-09-554-726A-20  
; Sequence 20, Application US/09554726A  
; Patent No. 6642369





2090 GGCTTCCAAAGAGGTGATGTTCCACGGAGGATGTCAGATTCTAC-----CTGGCTG 2143  
831 luleleuaspGlyLeuAlaTyrIleHisGluLysGlyMetIleHisArgAspLeuLysP 851  
2144 AGTGGCTTGGCTAGACCACTCCATCGGCTGGGATCATCTACAGGATCTGAAGC 2203  
851 roValAsnIlePheLeuAspSerAspHisValLysIleGlyAspPheGlyLeu--- 869  
2204 CAGAGATATCTCTGGATGAAGAGGACATATTAAAGATCACAGATTTGGCTTGACCA 2263  
870 -----AlaThrAspHis-----LeuAlaPheSerAlaAspSerLysGlnAspAspGlnT 886  
2264 AGGAGGCCACCGACCATGACAGAGAGCCCTATTCA----- 2298  
886 hrGlyAspLeuIleLysSerAspProSerGlyHisLeuThrGlyMetValGlyThrAlaL 906  
2299 -----TTTTGGGACTATTG 2314  
906 eutyValSerProGluVal-----GlnGlySerThrLysSerAlaTyrAsnGlnL 923  
2315 AATACATGGCGCCCGAGGTGGTGAACCGGCGTGGACACACACAGAGTGC----- 2364  
923 ysValAspLeuPheSerLeuGlyIlePhePheGluMetSerTyrHisProMetValT 943  
2365 -----GACTGTGTCTCTCGGTGTCTCTCATGTTCCAGATGCT-CAC----- 2405  
943 hrAlaSerGluArgIlePheValLeuAsnGlnLeuArgAspProThrSerProLysPheP 963  
2406 -----AGGGTCCCTGCCTCCATTCACAGGGGAAG 2430  
963 roGluAspPheAspAspGlyGluHisAlaLysGlnLys-----SerValIleSerT 980  
2431 GACAGGAAGAAACAATGGCCCGCATCTCAAGCAAGAAAGCTGGGTATGCTTGTTCCTC 2490  
980 rpLeuLeuAsnHisAspProAlaLysArgProThrAlaThrGluLeuLys----- 997  
2491 AGTGGCGAGGCTCAGAGCTCTCAGGGCCCTTTTCAAGCGGAACCCCTGCAACCGGCTA 2550  
998 -----SerGluLeuLeuProProGlnMetGluLysSerGluLeuHisGlu---V 1014  
2551 GGTAAAGGTCCCT-GTGACACCCCCACCCCCAG-----GAATCAATGAGGCTG 2597  
1014 alLeuHisHisThrLeuThrAsnValAspGly 1024  
2598 CCTCTAGACCCCTTAGGAATGTGAGAGCC 2629

RESULT 15  
US-09-803-671B-1  
; Sequence 1, Application US/09803671B  
; Patent No. 6582946  
; GENERAL INFORMATION:  
; APPLICANT: WEBSTER, Marion et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001161  
; CURRENT APPLICATION NUMBER: US/09/803,671B  
; CURRENT FILING DATE: 2001-03-12  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 4307  
; TYPE: DNA  
; ORGANISM: Human  
US-09-803-671B-1

Alignment Scores:  
Pred. No.: 8,6e-22 Length: 4307  
Score: 321.00 Matches: 128  
Percent Similarity: 38.13% Conservative: 100  
Best Local Similarity: 21.40% Mismatches: 210  
Query Match: 3.76% Indels: 160

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QY 119 GlyGluValMetIlePheGluLeuAlaTyrHisValGlnSerPheLeuSerGluHisAsn 138  
Db 2545 AGCGGAATTTAACTAATGATCTAGAGTTT-----GATAGTGTCTTCAGATCCTCT 2595  
QY 139 LysProProLysSerPheHisGluGluMetLeuGluArgAlaGlnGluGln 158  
Db 2596 AAAACACTTACAAATTTCTCTTCCAGCAAAACAGAAAGTGCATCTTCCAGACATAT 2655  
QY 159 GlnArgLeuLeuAlaLysArgLysGluGlnGlnArgGluLeuLeuHisGlu 178  
Db 2656 CAATATTGGGTACATTATTGGATCATGATAGTTAGCAAAATAAGTCAATCACATATCAA 2715  
QY 179 Ile-----GlnArgArgLysGluLeu 186  
Db 2716 ATGTTTGGAAAACCTTAAGTGGCAAAATTCATTTCCCAAGAAATTTATGACTCTGTA 2775  
QY 187 LysGluGluLysLysArgLysGluMetAlaLysGlnGluArgLeuGluLeuAlaSerLeu 206  
Db 2776 AATAATGAAGAAATTGACAGATGAATATTAGTTGTGTAGTCTCAGAAATTTATTAGTCTT 2835  
QY 207 SerAsnGlnAspHisThrSer-----LysLysAspProGlyGlyHis 220  
Db 2836 GATGAGAAAGATAACAACCTCTTGCCAAAAATGGCAATGAACAGATCTCTGAAAACCTTA 2895  
QY 221 ArgThrAlaIleLeuHisGlyGlySerProAspPheValGlyAsnGly----- 237  
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QY 238 ---LysHisArgAlaAsnSerSerGlyArgSer-----ArgArgGluArgGlnTyrSer 254  
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QY 255 ValCysAsn-----SerGluAspSerProGlySerCysGluLeuLeuTyr 269  
Db 3016 ATCTCAATGAAGAAGAGATATTTCTGAAATAGT----- 3051  
QY 270 PheAsnMetGlySerProAspGlnLeuMetValHisLysGlyLysCysIleGlySerAsp 289  
Db 3052 -----TTAAAGTCTGAAGAACCTATCTCTATGGACCAAGGGT----- 3087  
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QY 307 PheValLeuLeuTyrGluTrpValLeuGlnTrpGlnLysLysMetGlyProPheLeuThr 326  
Db 3148 CTAATAGCTGTAAACACAGCTGGCTTGGATACCTCTAATAAATTAGCT----- 3195  
QY 327 SerGlnGluLysGluLysIleAspLysCysLysIleGlnGlyThrGluThrGlu 346  
Db 3196 -----GCTGAAGAAGAAATACCGAAACTACAGGAGAA 3228  
QY 347 PheAsnSerLeuValLysLeuSerHisProAsnValValArgTyrLeuAlaMetAsnLeu 366  
Db 3229 GTAGATTCTCAAGGCATGAAACATGTCAACATTGTGGCTATTGTGGGACATGCTTG 3288  
QY 367 LysGluGlnAspAspSerIleValValAspIleLeuValGluHisIleSerGlyValSer 386  
Db 3289 CAAGAGAAAC-----ACTGTGAGCATTTTCAAGGATTTGTCTCTGTGGCTCA 3336  
QY 387 LeuAlaAlaHisLeuSerHisSerGlyProIleProValHisGlnLeuArgArgTyrThr 406  
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QY 407 AlaGlnLeuLeuSerGlyLeuAspTyrLeuHisSerAsnSerValValHisLysValLeu 426

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b 3397 AAACAATACCTTCAGGTTGCTTATCTCCATGAGAACTGTGTGTACATCGGATATC 3456
y 427 SerAlaSerAsnValLeuValaspAlaGluGlyThrValIleThrAspTyrSerIle 446
b 3457 AAAGGAATAATATGTTATGTCATGCAACTGGAATAATAAGCTGATTGCTTGGCTGT 3516
y 447 SerLysAspGluAla- 457
b 3517 GCCAGCGTTTGGCTGGCAGGTTTAATGGCACCCACAGTGCATGCTTAAG----- 3570
y 458 ValPheGluGlnThrArgValArgPheSerAspAsnAlaLeuProTyr----- 473
b 3571 -----TCCATGATGGACTCCATATTGGATGGGCCCA 3603
y 474 -----LysThrGlyLysLysGlyAspValTyrArgLeuGlyLeuLeu 487
b 3604 GAAGTCATCAATGAGTCGCTATGACGGAATCAGATATCTGGAGCATTTGTTGTTACT 3663
y 488 LeuLeuSerLeuSerGlnGlnGlu----- 496
b 3664 GTGTTTGAGATGGCTACAGGGAGGCTCCACTGGCTTCCATGGACAGGATGGCGGCATG 3723
y 497 -----CysGlyGluTyrProValThrIleProSerAspLeuProAlaAspPheGln--- 513
b 3724 TTTTACATCGAGACACCGAGGCTGATGCT---CCTTTACAGACCACTTCTCAGAA 3780
y 514 -----AspPheLeuLysLysCysValCysLeuAspAspLysGluArgTyrSerPro 530
b 3781 AATGCAGCAGACTTTTGTGGCATGTGCTGACCCAGGACCGACATGAGCGACCTTCTGCT 3840
y 531 GlnGlnLeuLeuLysHisSerPheIleAsnProGlnProLysMetProLeuValGluGln 550
b 3841 CTCGAGCTCTGAGACACTCTCTTTGGAGAGAACTCAGTGAATA----- 3885
y 551 SerProGluAspSerGlyGlyGlnAspTyrValGluThrVal-----IleProSerAsn 568
b 3886 -----TACATCAAGACTTTCTTCCAGTTCACACTGCAG 3918
y 569 ArgLeuProSerAlaAlaPhePheSerGluThrGlnArgGlnPheSerArgTyrPheIle 588
b 3919 ATGCTCCCTTGCTTAATTGGGGATGAT----- 3948
y 589 GluPheGluGlnLeuGlnLeuLeuGlyLysGlyAlaPheGlyAlaValIleLysValGln 608
b 3949 -----GGCTAAGGGATCTTTGTTTCCCCACTGAAATTCAG 3984
y 609 AsnLys-----LeuAspGlyCysCysTyr 616
b 3985 TCTAACCCAGTTAAGCAGATCCTATGGAGTCATTAACTGAAAGCTTGCAGTTAC 4038
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Search completed: March 22, 2004, 01:51:23  
Job time : 247 secs